

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 10, 2006, 23:10:21 ; Search time 32.1818 Seconds
(without alignments)
24.479 Million cell updates/sec

Title: US-10-825-603-2

Perfect score: 33

Sequence: 1 RXVSLSYR 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5 COMB.pcp.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6 COMB.pcp.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7 COMB.pcp.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H COMB.pcp.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/iaa/pCTUS COMB.pcp.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE COMB.pcp.*
- 7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	30	90.9	336 2	US-09-902-540-11471 Sequence 11471, A
2	29	87.9	9 2	US-09-646-193-2 Sequence 2, Appli
3	29	87.9	9 2	US-09-646-193-3 Sequence 3, Appli
4	29	87.9	9 2	US-09-646-192-2 Sequence 2, Appli
5	29	87.9	9 2	US-09-646-192-3 Sequence 3, Appli
6	29	87.9	10 2	US-09-646-193-4 Sequence 4, Appli
7	29	87.9	10 2	US-09-646-192-4 Sequence 4, Appli
8	29	87.9	264 2	US-09-902-540-9714 Sequence 9714, Ap
9	29	87.9	941 2	US-09-074-658-75 Sequence 75, Appl
10	28	84.8	18 2	US-09-430-470-18 Sequence 18, Appl
11	28	84.8	12 2	US-09-132-521-2 Sequence 2, Appli
12	28	84.8	14 2	US-09-543-940-10 Sequence 10, Appl
13	28	84.8	17 2	US-09-646-193-1 Sequence 1, Appli
14	28	84.8	17 2	US-09-646-192-1 Sequence 1, Appli
15	28	84.8	31 2	US-09-543-940-5 Sequence 5, Appli
16	28	84.8	32 2	US-09-144-838-12 Sequence 12, Appl
17	28	84.8	32 2	US-09-144-838-11 Sequence 11, Appl
18	28	84.8	33 2	US-09-144-838-14 Sequence 14, Appl
19	28	84.8	33 2	US-09-144-838-13 Sequence 13, Appl
20	28	84.8	66 2	US-09-144-838-27 Sequence 27, Appl
21	28	84.8	66 2	US-09-144-838-29 Sequence 29, Appl
22	28	84.8	66 2	US-09-144-838-35 Sequence 35, Appl
23	28	84.8	66 2	US-09-144-838-37 Sequence 37, Appl
24	28	84.8	67 2	US-09-144-838-8 Sequence 8, Appli
25	28	84.8	67 2	US-09-144-838-23 Sequence 23, Appl
26	28	84.8	67 2	US-09-144-838-25 Sequence 25, Appl

27	28	84.8	67 2	US-09-144-838-28	Sequence 28, Appl
28	28	84.8	67 2	US-09-144-838-30	Sequence 30, Appl
29	28	84.8	67 2	US-09-144-838-31	Sequence 31, Appl
30	28	84.8	67 2	US-09-144-838-33	Sequence 33, Appl
31	28	84.8	67 2	US-09-144-838-36	Sequence 36, Appl
32	28	84.8	67 2	US-09-144-838-38	Sequence 38, Appl
33	28	84.8	67 2	US-09-646-193-6	Sequence 6, Appli
34	28	84.8	67 2	US-09-646-192-6	Sequence 6, Appli
35	28	84.8	68 2	US-09-144-838-24	Sequence 24, Appl
36	28	84.8	68 2	US-09-144-838-26	Sequence 26, Appl
37	28	84.8	68 2	US-09-144-838-32	Sequence 32, Appl
38	28	84.8	68 2	US-09-144-838-34	Sequence 34, Appl
39	28	84.8	68 2	US-09-175-713-14	Sequence 14, Appl
40	28	84.8	69 2	US-09-175-713-10	Sequence 10, Appl
41	28	84.8	72 2	US-09-175-713-15	Sequence 15, Appl
42	28	84.8	72 2	US-09-646-193-7	Sequence 7, Appli
43	28	84.8	72 2	US-09-646-192-7	Sequence 7, Appli
44	28	84.8	73 2	US-09-175-713-11	Sequence 11, Appl
45	28	84.8	81 2	US-09-248-796A-24270	Sequence 24270, A

ALIGNMENTS

RESULT 1

US-09-902-540-11471
; Sequence 11471, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 11471
; LENGTH: 336
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-11471

Query Match 90.9%; Score 30; DB 2; Length 336;
Best Local Similarity 75.0%; Pred. No. 92;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RXVSLSYR 8
| | | | |
Db 35 RAVSLNYR 42

RESULT 2

US-09-646-193-2
; Sequence 2, Application US/09646193
; Patent No. 6875738
; GENERAL INFORMATION:
; APPLICANT: Clark-Lewis, Ian
; APPLICANT: Duronio, Vincent
; APPLICANT: Salari, Hassan
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: Therapeutic Chemokine Receptor Antagonists
; FILE REFERENCE: 080353-000000US
; CURRENT APPLICATION NUMBER: US/09/646,193
; CURRENT FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: CA 2,245,224
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: WO PCT/CA99/00221
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: WO PCT/CA99/00750

; PRIOR FILING DATE: 1999-08-16
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:CXCR4
; OTHER INFORMATION: antagonist peptide compound N-terminal sequence
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (9)
; OTHER INFORMATION: Xaa = Cys or Cys modified by a polypeptide
; OTHER INFORMATION: homologous to a portion of SDF-1
US-09-646-193-2

Query Match 87.9%; Score 29; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 5e+05;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RXVLSLSYR 8
: |||||
Db 1 KGVLSLSYR 8

RESULT 3
US-09-646-193-3
; Sequence 3, Application US/09646193
; Patent No. 6875738
; GENERAL INFORMATION:
; APPLICANT: Clark-Lewis, Ian
; APPLICANT: Duttonio, Vincent
; APPLICANT: Salari, Hassan
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: Therapeutic Chemokine Receptor Antagonists
; FILE REFERENCE: 080353-000000US
; CURRENT APPLICATION NUMBER: US/09/646,193
; CURRENT FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: CA 2,245,224
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: WO PCT/CA99/00221
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: WO PCT/CA99/00750
; PRIOR FILING DATE: 1999-08-16
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:CXCR4
; OTHER INFORMATION: antagonist peptide compound of dimerized
; OTHER INFORMATION: N-terminal amino acid sequence SDF-1(1-8)-2
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (9)
; OTHER INFORMATION: Xaa = any brige forming moiety, such as ornithine or
; OTHER INFORMATION: L-amino-N-butyric acid in which two amino groups are used to form
; OTHER INFORMATION: linkage between dimerized SDF-1(1-8)-2, or Lys, where the epsilon
; OTHER INFORMATION: amino group forms an amide bond to Arg in the peptide
; OTHER INFORMATION: Arg-Tyr-Ser-Leu-Ser-Val-Gly-Lys, represented from the carboxyl to
; OTHER INFORMATION: amino end
US-09-646-193-3

Query Match 87.9%; Score 29; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 5e+05;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RXVLSLSYR 8
: |||||
Db 1 KGVLSLSYR 8

RESULT 4
US-09-646-192-2
; Sequence 2, Application US/09646192
; Patent No. 6946445
; GENERAL INFORMATION:
; APPLICANT: Clark-Lewis, Ian
; APPLICANT: Gong, Jiang-Hong
; APPLICANT: Duttonio, Vincent
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: Therapeutic Chemokine Receptor Antagonists
; FILE REFERENCE: 080352-000000US
; CURRENT APPLICATION NUMBER: US/09/646,192
; CURRENT FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: CA 2,226,391
; PRIOR FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: CA 2,245,224
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: WO PCT/CA99/00221
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:CXCR4
; OTHER INFORMATION: antagonist peptide compound N-terminal sequence
; NAME/KEY: MOD_RES
; LOCATION: (9)
; OTHER INFORMATION: Xaa = Cys or Cys modified by a polypeptide
; OTHER INFORMATION: homologous to a portion of SDF-1
US-09-646-192-2

Query Match 87.9%; Score 29; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 5e+05;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RXVLSLSYR 8
: |||||
Db 1 KGVLSLSYR 8

RESULT 5
US-09-646-192-3
; Sequence 3, Application US/09646192
; Patent No. 6946445
; GENERAL INFORMATION:
; APPLICANT: Clark-Lewis, Ian
; APPLICANT: Gong, Jiang-Hong
; APPLICANT: Duttonio, Vincent
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: Therapeutic Chemokine Receptor Antagonists
; FILE REFERENCE: 080352-000000US
; CURRENT APPLICATION NUMBER: US/09/646,192
; CURRENT FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: CA 2,226,391
; PRIOR FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: CA 2,245,224
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: WO PCT/CA99/00221
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:CXCR4
; OTHER INFORMATION: antagonist peptide compound of dimerized

```
; OTHER INFORMATION: N-terminal amino acid sequence
; NAME/KEY: MOD RES
; LOCATION: (9)
; OTHER INFORMATION: Xaa = Lys, where the epsilon amino group forms an
; OTHER INFORMATION: amide bond to Arg in the peptide
; OTHER INFORMATION: Arg-Tyr-Ser-Leu-Ser-Val-Gly-Lys, represented from
; OTHER INFORMATION: the carboxyl to amino end
US-09-646-192-3

Query Match      87.9%; Score 29; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 5e+05;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RXVSLSYR 8
   : |||||
Db 1 KGVSLSYR 8

RESULT 6
US-09-646-193-4
; Sequence 4, Application US/09646193
; Patent No. 6875738
; GENERAL INFORMATION:
; APPLICANT: Clark-Lewis, Ian
; APPLICANT: Duronio, Vincent
; APPLICANT: Salari, Hassan
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: Therapeutic Chemokine Receptor Antagonists
; FILE REFERENCE: 080353-000000US
; CURRENT APPLICATION NUMBER: US/09/646,193
; CURRENT FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: CA 2,245,224
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: WO PCT/CA99/00221
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: WO PCT/CA99/00750
; PRIOR FILING DATE: 1999-08-16
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 4
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CXCR4
; OTHER INFORMATION: antagonist peptide compound of dimerized
; OTHER INFORMATION: N-terminal amino acid sequence SDF-1(1-9)-2
; NAME/KEY: MOD RES
; LOCATION: (10)
; OTHER INFORMATION: Xaa = any brige forming moiety, such as ornithine or
; OTHER INFORMATION: L-amino-N-butyric acid in which two amino groups are
; OTHER INFORMATION: linkage between dimerized SDF-1(1-9)-2, or Lys, where the epsilon
; OTHER INFORMATION: amino group forms an amide bond to Arg in the peptide
; OTHER INFORMATION: Cys-Arg-Ser-Leu-Ser-Val-Gly-Lys, represented from the carboxyl to
; OTHER INFORMATION: amino end
US-09-646-193-4

Query Match      87.9%; Score 29; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 3.7;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RXVSLSYR 8
   : |||||
Db 1 KGVSLSYR 8

RESULT 7
US-09-646-192-4
; Sequence 4, Application US/09646192
; Patent No. 6946445
; GENERAL INFORMATION:
; APPLICANT: Clark-Lewis, Ian
```

```
; APPLICANT: Gong, Jiang-Hong
; APPLICANT: Duronio, Vincent
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: Therapeutic Chemokine Receptor Antagonists
; FILE REFERENCE: 080352-000000US
; CURRENT APPLICATION NUMBER: US/09/646,192
; CURRENT FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: CA 2,226,391
; PRIOR FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: CA 2,245,224
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: WO PCT/CA99/00221
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 4
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CXCR4
; OTHER INFORMATION: antagonist peptide compound of dimerized
; OTHER INFORMATION: N-terminal amino acid sequence
; NAME/KEY: MOD RES
; LOCATION: (10)
; OTHER INFORMATION: Xaa = Lys, where the epsilon amino group forms an
; OTHER INFORMATION: amide bond to Cys in the peptide
; OTHER INFORMATION: Cys-Arg-Ser-Leu-Ser-Val-Gly-Lys, represented from
; OTHER INFORMATION: the carboxyl to amino end
US-09-646-192-4

Query Match      87.9%; Score 29; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 3.7;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RXVSLSYR 8
   : |||||
Db 1 KGVSLSYR 8

RESULT 8
US-09-902-540-9714
; Sequence 9714, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 9714
; LENGTH: 264
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-9714

Query Match      87.9%; Score 29; DB 2; Length 264;
Best Local Similarity 75.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RXVSLSYR 8
   : |||||
Db 91 RRVSLTYR 98

RESULT 9
US-09-074-658-75
```

; Sequence 75, Application US/09074658
; Patent No. 6184371
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M
; APPLICANT: Run-Pan Du
; APPLICANT: Quijun Wang
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Klein, Michel H
; TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/074,658
; FILING DATE: 08-MAY-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-795
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 75:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 941 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-074-658-75

Query Match 87.9%; Score 29; DB 2; Length 941;
Best Local Similarity 75.0%; Pred. No. 4.5e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RXVLSYSR 8
Db 660 RHLSLSYR 667

RESULT 10
US-09-430-470-18
; Sequence 18, Application US/09430470
; Patent No. 6562800
; GENERAL INFORMATION:
; APPLICANT: McMillan, Minnie
; TITLE OF INVENTION: THE USE OF IMMUNOPOTENTIATING SEQUENCES
; TITLE OF INVENTION: FOR INDUCING IMMUNE RESPONSE
; FILE REFERENCE: 13761-725
; CURRENT APPLICATION NUMBER: US/09/430,470
; CURRENT FILING DATE: 1999-10-29
; EARLIER APPLICATION NUMBER: US 60/106,506
; EARLIER FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-430-470-18
Query Match 84.8%; Score 28; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3 VLSYSR 8
Db 3 VLSYSR 8

RESULT 11
US-09-132-521-2
; Sequence 2, Application US/09132521
; Patent No. 6828138
; GENERAL INFORMATION:
; APPLICANT: Nagai, Yoshiyuki
; APPLICANT: Shioda, Tatsuo
; APPLICANT: Moriya, Chikaya
; TITLE OF INVENTION: Recombinant sendai virus vector
; TITLE OF INVENTION: comprising a gene encoding chemokine
; FILE REFERENCE: 50026/008001
; CURRENT APPLICATION NUMBER: US/09/132,521
; CURRENT FILING DATE: 1998-08-11
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 9, 11
; OTHER INFORMATION: Xaa is predicted to be Cys
US-09-132-521-2

Query Match 84.8%; Score 28; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 7.3; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 VLSYSR 8
Db 3 VLSYSR 8

RESULT 12
US-09-543-940-10
; Sequence 10, Application US/09543940
; Patent No. 6613742
; GENERAL INFORMATION:
; APPLICANT: Huang, Ziwei
; APPLICANT: Luo, Zhaowen
; APPLICANT: Zhou, Naiming
; APPLICANT: Luo, Jiansong
; TITLE OF INVENTION: Chemokine-Derived Synthetic Peptides
; FILE REFERENCE: 8321-40
; CURRENT APPLICATION NUMBER: US/09/543,940
; CURRENT FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/128,106
; PRIOR FILING DATE: 1999-04-07
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 10
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide containing segment from N-terminal region
; OTHER INFORMATION: of human SDF-1 protein
US-09-543-940-10

Query Match 84.8%; Score 28; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 8.6; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 VLSYSR 8


```
Db          3 VLSYSR 8
|||||
Query Match      84.8%; Score 28; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 13
US-09-646-193-1
; Sequence 1, Application US/09646193
; Patent No. 6875738
; GENERAL INFORMATION:
; APPLICANT: Clark-Lewis, Ian
; APPLICANT: Duronio, Vincent
; APPLICANT: Salari, Hassan
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: Therapeutic Chemokine Receptor Antagonists
; FILE REFERENCE: 080353-000000US
; CURRENT APPLICATION NUMBER: US/09/646,193
; CURRENT FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: CA 2,245,224
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: WO PCT/CA99/00221
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: WO PCT/CA99/00750
; PRIOR FILING DATE: 1999-08-16
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:two putative
; OTHER INFORMATION: CXCR4 binding sites joined by the CXC motif
US-09-646-193-1

Query Match      84.8%; Score 28; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          3 VLSYSR 8
|||||
Db          3 VLSYSR 8
|||||

RESULT 14
US-09-646-192-1
; Sequence 1, Application US/09646192
; Patent No. 6946445
; GENERAL INFORMATION:
; APPLICANT: Clark-Lewis, Ian
; APPLICANT: Gong, Jiang-Hong
; APPLICANT: Duronio, Vincent
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: Therapeutic Chemokine Receptor Antagonists
; FILE REFERENCE: 080352-000000US
; CURRENT APPLICATION NUMBER: US/09/646,192
; CURRENT FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: CA 2,226,391
; PRIOR FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: CA 2,245,224
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: WO PCT/CA99/00221
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:two putative
; OTHER INFORMATION: CXCR4 binding sites joined by the CXC motif
US-09-646-192-1

Query Match      84.8%; Score 28; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          3 VLSYSR 8
|||||
Db          3 VLSYSR 8
|||||

RESULT 15
US-09-543-940-5
; Sequence 5, Application US/09543940
; Patent No. 6613742
; GENERAL INFORMATION:
; APPLICANT: Huang, Ziwei
; APPLICANT: Luo, Zhaowen
; APPLICANT: Zhou, Naiming
; APPLICANT: Luo, Jiansong
; TITLE OF INVENTION: Chemokine-Derived Synthetic Peptides
; FILE REFERENCE: 8321-40
; CURRENT APPLICATION NUMBER: US/09/543,940
; CURRENT FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/128,106
; PRIOR FILING DATE: 1999-04-07
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide containing segments from N- and C-terminal
; OTHER INFORMATION: regions of human SDF-1 protein
US-09-543-940-5

Query Match      84.8%; Score 28; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          3 VLSYSR 8
|||||
Db          3 VLSYSR 8
|||||

Search completed: August 10, 2006, 23:13:10
Job time : 33.1818 secs
```

THIS PAGE BLANK (USPTO)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

QM protein - protein search, using sw model

Run on: August 10, 2006, 22:53:25 ; Search time 150 Seconds
(without alignments)
55.501 Million cell updates/sec

Title: US-10-825-603-2

Perfect score: 33

Sequence: 1 RXVSLSYRX 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 7.2.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	93.9	189	2	Q4CAP4_CROWT
2	31	93.9	301	2	Q6SHY0_9BACT
3	30	90.9	433	2	Q2S253_SAPHI
4	30	90.9	836	2	Q7S620_NEUCR
5	30	90.9	863	2	O83303_TREPA
6	29	87.9	196	2	Q9PC62_XYLFA
7	29	87.9	217	2	Q87D15_XYLFT
8	29	87.9	221	2	Q7QUP1_GIALA
9	29	87.9	230	2	Q8L2F0_AZOBR
10	29	87.9	254	2	Q6LIC6_PICTO
11	29	87.9	264	2	Q2JYN7_RHJET
12	29	87.9	239	2	Q9RBF7_RALEU
13	29	87.9	315	2	Q3FW00_9DELT
14	29	87.9	355	2	Q6NXAS_BRARE
15	29	87.9	356	2	Q66JN5_BRARE
16	29	87.9	406	2	Q47YI2_COLP3
17	29	87.9	413	2	Q4ZV36_PSEU2
18	29	87.9	647	2	Q47VZ6_COLP3
19	29	87.9	940	2	Q51187_NEIME
20	29	87.9	2405	2	Q8L3E9_STRPN
21	28	84.8	24	1	HPTA_RABIT
22	28	84.8	89	1	SDF1_MOUSE
23	28	84.8	89	2	Q6ICW0_HUMAN
24	28	84.8	89	2	Q3LSL5_CANFA
25	28	84.8	89	2	Q5XNN9_CANFA
26	28	84.8	89	2	Q8HYPO_MACMU
27	28	84.8	89	2	Q543V6_MOUSE
28	28	84.8	89	2	Q9QZD1_RAT
29	28	84.8	90	2	Q2L986_HUMAN
30	28	84.8	92	2	Q9H554_HUMAN
31	28	84.8	93	1	SDF1_FELCA

32	28	84.8	93	1	SDF1_HUMAN
33	28	84.8	93	2	Q3LSL4_CANFA
34	28	84.8	93	2	Q5R8M6_PONPY
35	28	84.8	93	2	Q4FJL5_MOUSE
36	28	84.8	100	2	Q2L985_HUMAN
37	28	84.8	116	2	Q6EKW4_PIG
38	28	84.8	119	2	Q5IT36_HUMAN
39	28	84.8	119	2	Q80YV8_RAT
40	28	84.8	140	2	Q2L988_HUMAN
41	28	84.8	150	2	Q8BPB7_MOUSE
42	28	84.8	157	2	Q3VUS1_PROAE
43	28	84.8	157	2	Q8D9U8_VIBVU
44	28	84.8	169	2	Q6NBB1_RHOPA
45	28	84.8	172	2	Q5GD95_XENNE

P48061	homo sapien
Q3LSI4	canis famli
Q5R8M6	pongo pygma
Q4FJL5	mus musculus
Q2L985	homo sapien
Q6EKW4	eus acrofa
Q5IT36	homo sapien
Q80YV8	rattus norv
Q2L988	homo sapien
Q8BPB7	m 11 days p
Q3VUS1	prosthococh
Q8D9U8	vibrio vuln
Q6NBB1	rhodopsendo
Q5GD95	xenorhabdus

ALIGNMENTS

RESULT 1
Q4CAP4_CROWT PRELIMINARY; PRT; 189 AA.
AC Q4CAP4;
DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 13-SEP-2005, sequence version 1.
DT 07-FEB-2006, entry version 2.
DE Hypothetical protein.
DE ORFNames=CwatDRAFT 6100;
GN Crocospaera watsonii.
OC Bacteria; Cyanobacteria; Chroococcales; Crocospaera.
OX NCBI_TaxID=165597;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=WH 8501;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RA "Sequencing of the draft genome and assembly of Crocospaera watsonii
RT WH 8501."
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=WH 8501;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RA "Annotation of the draft genome assembly of Crocospaera watsonii WH
RT 8501."
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=WH 8501;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RA Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC EMBL; AADV02000001; EMB2892.1; -; Genomic_DNA.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0006935; P:chemotaxis; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR002545; Chew.
KW Hypothetical protein.
SQ SEQUENCE 189 AA; 21072 MW; 9459EE83CB0752B CRC64;

Query Match 93.9%; Score 31; DB 2; Length 189;
Best Local Similarity 87.5%; Pred. No. 55;

```
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 RXVSLSYR 8
Db 139 RPSVLSYR 146

RESULT 2
Q6SHY0_9BACT PRELIMINARY; PRT; 301 AA.
AC Q6SHY0;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Hypothetical protein.
GN ORFNames=EBAC750-01B07.33;
OS uncultured bacterium 106.
OC Bacteria; environmental samples.
OX NCBI_TaxID=257383;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RA DeLong E.F.;
RT "Monterey Bay Coastal Ocean Microbial Observatory environmental clone
sequencing.";
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
RN (2)
RP NUCLEOTIDE SEQUENCE.
RA Heidelberg J.F., Eisen J.A., Nelson W.C., DeLong E.F.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AY458630; AAR37491.1; -; Genomic_DNA.
DR InterPro; IPR003390; DUF147.
DR Pfam; PF02457; DUF147; 1.
DR TIGRFAMs; TIGR00159; DUF147; 1.
SQ SEQUENCE 301 AA; 33566 MW; 59CFFC1B871F5D37 CRC64;

Query Match 93.9%; Score 31; DB 2; Length 301;
Best Local Similarity 75.0%; Pred. No. 91;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RXVSLSYR 8
Db 227 REISLSYR 234

RESULT 3
Q2S253_9SPHI PRELIMINARY; PRT; 433 AA.
AC Q2S253;
DT 24-JAN-2006, integrated into UniProtKB/TrEMBL.
DT 24-JAN-2006, sequence version 1.
DT 07-MAR-2006, entry version 3.
DE DnaJ domain protein.
GN ORFNames=SRU_1607;
OS Salinibacter ruber DSM 13855.
OC Bacteria; Bacteroidetes; Sphingobacteriales;
OC Crenotrichaceae; Salinibacter.
OX NCBI_TaxID=309807;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DSM 13855;
RX PubMed=16330755; DOI=10.1073/pnas.0509073102;
RA Mongodin E.F., Nelson K.E., Daugherty S., Deboy R.T., Wister J.,
RA Khouri H., Weidman J., Walsh D.A., Papke R.T., Sanchez Perez G.,
RA Sharma A.K., Nesbo C.L., MacLeod D., Baptiste E., Doolittle W.F.,
RA Charlebois R.L., Legault B., Rodriguez-Valera F.;
RT "The genome of Salinibacter ruber: Convergence and gene exchange among
hyperhalophilic bacteria and archaea.";
RL Proc. Natl. Acad. Sci. U.S.A. 102:18147-18152(2005).
```

```
CC -! SUBCELLULAR LOCATION: Membrane-bound. Mitochondrial; inner
CC membrane (By similarity).
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; CP000159; ABC43940.1; -; Genomic_DNA.
KW Chapter: Inner membrane; Membrane; Protein transport; Translocation;
KW Transmembrane; Transport.
SQ SEQUENCE 433 AA; 48388 MW; 6E8C151D56CB50E1 CRC64;

Query Match 90.9%; Score 30; DB 2; Length 433;
Best Local Similarity 75.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RXVSLSYR 8
Db 185 RSVLSYR 192

RESULT 4
Q7S620_NEUCR PRELIMINARY; PRT; 836 AA.
AC Q7S620;
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 15-DEC-2003, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Predicted protein.
GN ORFNames=NCU05640.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN (1)
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=74-OR23-1A / FGSC 987;
RX MEDLINE=22598136; PubMed=12712197; DOI=10.1038/nature01554;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehm B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Ianakiev P., Bell-Pedersen D., Nelson M.A.,
RA Werner-Washburne M., Selitrennikoff C.P., Kinsey J.A., Braun E.L.,
RA Zelter A., Schulte U., Kothe G.O., Jedd G., Mewes H.-W., Staben C.,
RA Marcotte E., Greenberg D., Roy A., Foley K., Naylor J.,
RA Stange-Thomann N., Barrett R., Gnerre S., Kamal M., Kamvysselis M.,
RA Mauceli E., Bielke C., Rudd S., Frisman D., Krystofova S.,
RA Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S., Cogoni C.,
RA Macino G., Catchside D.E.A., Li W., Pratt R.J., Osmari S.A.,
RA DeSouza C.P.C., Glass N.L., Orbach M.J., Berglund J.A., Voelker R.,
RA Yarden O., Plamann M., Seiler S., Dunlap J.C., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nuebaum C., Birren B.W.;
RT "The genome sequence of the filamentous fungus Neurospora crassa.";
RL Nature 422:859-868(2003).
CC
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AABX01000332; EAA30965.1; -; Genomic_DNA.
DR InterPro; IPR007087; Znf_C2H2.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; UNKNOW1.
SQ SEQUENCE 836 AA; 91692 MW; 7D3858CE2EF435F7 CRC64;

Query Match 90.9%; Score 30; DB 2; Length 836;
Best Local Similarity 75.0%; Pred. No. 4.8e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RXVSLSYR 8
Db 536 RLVSISYR 543
```

```

RESULT 5
O83303 TREPA PRELIMINARY; PRT; 863 AA.
ID O83303 TREPA PRELIMINARY; PRT; 863 AA.
AC O83303;
DT 01-NOV-1998, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1998, sequence version 1.
DT 07-FEB-2006, entry version 25.
DE Ribosomal protein S1 (RpsA).
DE OrderedLocusNames=TP0279; ORFNames=TP_0279;
OS Treponema pallidum.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
OC NCBI_TaxID=160;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Nichols;
RX MEDLINE=98332770; PubMed=9665876; DOI=10.1126/science.281.5375.375;
RA Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
RA Dodson R.J., Winn M.L., Hickey E.K., Clayton R.A., Ketchum K.A.,
RA Sodergren E., Hardham J.M., McLeod M.P., Salzberg S.L., Peterson J.D.,
RA Khalak H.G., Richardson D.L., Howell J.K., Chidambaram M.,
RA Uterback T.R., McDonald L.A., Artlach P., Bowman C., Cotton M.D.,
RA Fujii C., Garland S.A., Hatch B., Horst K., Roberts K.M., Sandusky M.,
RA Weidman J.F., Smith H.O., Venter J.C.;
RT "Complete genome sequence of Treponema pallidum, the syphilis
RT spirochete.";
RL Science 281:375-388(1998).
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
EMBL; AB000520; AAC65266.1; -; Genomic_DNA.
DR EPI; B71343; B71343.
DR HSP; P05055; LSRO.
DR TIGR; TP0279; -.
DR GO; GO:0005840; C:ribosome; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004127; F:cyclidylate kinase activity; IEA.
DR GO; GO:0003723; F:rRNA binding; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR GO; GO:0006139; P:nucleobase, nucleoside, nucleotide and nucl. .; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR InterPro; IPR011769; Ad Ct kin N.
DR InterPro; IPR003136; Cyclidylate kin.
DR InterPro; IPR011994; Cyclidylate kin_d.
DR InterPro; IPR012340; OB NA bd sub.
DR InterPro; IPR000110; Ribosomal_S1.
DR InterPro; IPR003029; S1_RNA_bd.
DR Pfam; PF02224; Cyclidylate_kin; 1.
DR Pfam; PF00575; S1; 5.
DR PRINTS; PR00681; RIBOSOMALS1.
DR ProDom; PD000657; Adenylate_kin; 1.
DR SMART; SM00316; S1; 6.
DR TIGRfams; TIGR00017; cmk; 1.
DR TIGRfams; TIGR00717; rpsA; 1.
DR PROSITE; PS0126; S1; 6.
KW Complete proteome; Ribosomal protein.
SQ SEQUENCE 863 AA; 95563 MW; 1BBA56BBA07A6319 CRC64;

Query Match 90.9%; Score 30; DB 2; Length 863;
Best Local Similarity 75.0%; Pred. No. 56+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RXVLSYSR 8
DB 135 RTVALSYSR 142

RESULT 6
O9PC62 XYLFA PRELIMINARY; PRT; 196 AA.
ID O9PC62 XYLFA PRELIMINARY; PRT; 196 AA.
AC O9PC62;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Iron-sulfur flavoprotein.
DE Name=isf; OrderedLocusNames=PD0872; ORFNames=PD_0872;
OS Xylella fastidiosa (strain Temecula / ATCC 700964).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xylella.

```

```

DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2000, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE Hypothetical protein.
GN OrderedLocusNames=Xf1919;
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xylella.
OX NCBI_TaxID=2371;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=9a5C;
RX MEDLINE=20365717; PubMed=10910347; DOI=10.1038/35018003;
RA Simpson A.G., Reinach F.C., Arruda E., Abreu F.A., Acencio M.,
RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,
RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Matsukuma A.Y.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tshako M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
RT "The genome sequence of the plant pathogen Xylella fastidiosa.";
RL Nature 406:151-159(2000).
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
EMBL; AE004011; AAF84725.1; -; Genomic_DNA.
DR EPI; G82622; G82622.
DR InterPro; IPR005025; FMN_red.
DR Pfam; PF03358; FMN_red; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 196 AA; 22065 MW; B7301147088F7844 CRC64;

Query Match 87.9%; Score 29; DB 2; Length 196;
Best Local Similarity 62.5%; Pred. No. 1.7e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RXVLSYSR 8
DB 176 RMISYSR 183

RESULT 7
O87D15 XYLFT PRELIMINARY; PRT; 217 AA.
ID O87D15 XYLFT PRELIMINARY; PRT; 217 AA.
AC O87D15;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Iron-sulfur flavoprotein.
DE Name=isf; OrderedLocusNames=PD0872; ORFNames=PD_0872;
OS Xylella fastidiosa (strain Temecula / ATCC 700964).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xylella.

```

OX NCBI_TaxID=183190;
RN [1]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=22421331; PubMed=12533478;
RX DOI=10.1128/JB.185.3.1018-1026.2003;
RA Van Sluys M.A., de Oliveira M.C., Monteiro-Vitorello C.B.,
RA Mayaki C.F., Furlan L.R., Camargo L.E.A., da Silva A.C.R., Moon D.H.,
RA Takita M.A., Lemos E.G.M., Machado M.A., Ferro M.T., da Silva F.R.,
RA Goldman M.H.S., Goldman G.H., Lemos M.V.F., El-Dorri H., Tsai S.M.,
RA Carver H., Carraro D.M., de Oliveira R.C., Nunes L.R., Siqueira W.J.,
RA Coutinho L.L., Kimura E.T., Ferro E.S., Harakava R., Kuramae E.E.,
RA Marino C.L., Gidlietti E., Abreu I.L., Alves L.M.C., do Amaral A.M.,
RA Baia G.S., Bianco S.R., Brito M.S., Cannavan F.S., Celestino A.V.,
RA da Cunha A.F., Fenille R.C., Ferro J.A., Formighieri E.F., Kishi L.T.,
RA Leoni S.G., Oliveira A.R., Rosa V.E. Jr., Sasaki F.T., Sena J.A.D.,
RA de Souza A.A., Truffi D., Tsukumo F., Yanai G.M., Zatos L.G.,
RA Civerolo E.L., Simpson A.J.G., Almeida N.F. Jr., Setubal J.C.,
RA Kitajima J.P.;
RT "Comparative analyses of the complete genome sequences of Pierce's
RT disease and citrus variegated chlorosis strains of Xylella
RT fastidiosa";
RL J. Bacteriol. 185:1018-1026 (2003).
CC -----
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL; AE009442; AA028739.1; -; Genomic_DNA.
DR BIOCyc; XPAS183190.PD0872-MONOMER; -;
DR InterPro; IPR005025; FNN red.
DR Pfam; PF03358; FNN_red; 1.
KW Complete proteome.
SQ SEQUENCE 217 AA; 24262 MW; 10BB82B728F83412 CRC64;

Query Match 87.9%; Score 29; DB 2; Length 217;
Best Local Similarity 62.5%; Pred. No. 2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RXVSLSYR 8
| :|:|:|
DB 197 RMISISYR 204

RESULT 8
Q7QUP1 GIALA PRELIMINARY; PRT; 221 AA.
AC Q7QUP1;
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 15-DEC-2003, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE GLP 47 31579 30914.
OS Giardia lamblia ATCC 50803.
OC Eukaryota; Diplomonadida; Hexamitidae; Giardinales; Giardia.
OX NCBI_TaxID=184922;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=WB C6;
RC Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
RA Olsen G.J., Sogin M.L.;
RT "Draft sequence of the Giardia lamblia genome.";
RL submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL; AACB01000091; EAA38771.1; -; Genomic DNA.
DR SEQUENCE 221 AA; 24100 MW; 3BADB35C6A920D37 CRC64;

Query Match 87.9%; Score 29; DB 2; Length 221;
Best Local Similarity 75.0%; Pred. No. 2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
 DR GO; GO:0006412; P:protein biosynthesis; IEA.
 DR InterPro; IPR002136; Ribosomal_L4/LiE.
 DR Pfam; PF00573; Ribosomal_L4; 1.
 KW Complete proteome; Ribosomal protein.
 SQ SEQUENCE 254 AA; 28264 MW; 2273574810CD85B3 CRC64;

Query Match 87.9%; Score 29; DB 2; Length 254;
 Best Local Similarity 82.5%; Pred. No. 2.3e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RXVLSYSR 8
 | :|||||
 Db 36 RAITLSYR 43

RESULT 11

ID Q2JYN7_RHIET PRELIMINARY; PRT; 264 AA.
 AC Q2JYN7_RHIET
 DT 07-MAR-2006, integrated into UniProtKB/TrEMBL.
 DT 07-MAR-2006, sequence version 1.
 DE Putative pyroline-5-carboxylate reductase protein.
 GN ORFNames=RHE PF00409;
 OS Rhizobium etli CFN 42.
 OG Plasmid p42f.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Rhizobiaceae; Rhizobium.
 OX NCBI_TaxID=347834;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=CFN 42;
 RA Gonzalez V., Santamaria R.I., Bustos P., Hernandez-Gonzalez I.,
 RA Medrano-Soto A., Moreno-Hagelsieb G., Chandra-Janga S.,
 RA Ramirez-Romero M.A., Collado-Vides J., Davila G.;
 RL Submitted (SEP-2005) to the EMBL/GenBank/DBJ databases.
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC EMBL; EMBL; ABC94299.1; -; Genomic_DNA.
 DR Plasmid.
 KW Plasmid.
 SQ SEQUENCE 264 AA; 27858 MW; 0F008E95A47D2100 CRC64;

Query Match 87.9%; Score 29; DB 2; Length 264;
 Best Local Similarity 75.0%; Pred. No. 2.4e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RXVLSYSR 8
 | :|||||
 Db 33 RNLISYR 40

RESULT 12

Q9RBF7_RALEU PRELIMINARY; PRT; 299 AA.
 AC Q9RBF7;
 DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
 DT 01-MAY-2000, sequence version 1.
 DT 07-FEB-2006, entry version 22.
 DE Formate dehydrogenase.
 GN Name=fdsR;
 OS Ralstonia eutropha (Alcaligenes eutrophus).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Burkholderiaceae; Cupriavidus.
 OX NCBI_TaxID=106590;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=H16;
 RA MEDLINE=20032351; PubMed=10564479;
 RX Oh J.I., Bowien B.;

RT "Dual control by regulatory gene fdsR of the fds operon encoding the

RT NAD(+)-linked formate dehydrogenase of Ralstonia eutropha.";
 RL Mol. Microbiol. 34:365-376(1999).
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC EMBL; AJ007718; CAB59983.1; -; Genomic_DNA.
 DR HSSP; P46930; 107L.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR GO; GO:0006350; P:transcription; IEA.
 DR InterPro; IPR000847; HTH_LYAR.
 DR InterPro; IPR011991; Wing_hlx_DNA_bd.
 DR Pfam; PF00126; HTH_1; 1.
 KW DNA-binding; Transcription; Transcription regulation.
 SQ SEQUENCE 299 AA; 32320 MW; 43DD1AD3D40CA4BC CRC64;

Query Match 87.9%; Score 29; DB 2; Length 299;
 Best Local Similarity 75.0%; Pred. No. 2.8e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RXVLSYSR 8
 | :|||||
 Db 46 QAVLSYSR 53

RESULT 13

ID Q3FYW0_9DELT PRELIMINARY; PRT; 315 AA.
 AC Q3FYW0;
 DT 08-NOV-2005, integrated into UniProtKB/TrEMBL.
 DT 08-NOV-2005, sequence version 1.
 DT 07-FEB-2006, entry version 3.
 DE Hypothetical protein.
 GN ORFNames=ProBRAFT_0503;
 OS Pelobacter propionicus DSM 2379.
 OC Bacteria; Proteobacteria; Deitaproteobacteria; Desulfuromonadales;
 OC Pelobacteraceae; Pelobacter.
 OX NCBI_TaxID=338966;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=DSM 2379;
 RG US DOE Joint Genome Institute (JGI-PGF);
 RA Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T.,
 RA Hammon N., Istrani S., Pitluck S., Richardson P.;
 RT "Sequencing of the draft genome and assembly of Pelobacter propionicus
 DSM 2379.";
 RL Submitted (AUG-2005) to the EMBL/GenBank/DBJ databases.
 RN [2]

RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=DSM 2379;
 RG US DOE Joint Genome Institute (JGI-ORNL);
 RA Larimer F., Land M.;
 RT "Annotation of the draft genome assembly of Pelobacter propionicus DSM
 2379.";
 RL Submitted (AUG-2005) to the EMBL/GenBank/DBJ databases.
 CC !- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.

CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC EMBL; AAJH01000025; EAO35065.1; -; Genomic_DNA.
 DR Hypothetical protein.
 SQ SEQUENCE 315 AA; 35865 MW; 47D00D3E6C74C4AE CRC64;

Query Match 87.9%; Score 29; DB 2; Length 315;
 Best Local Similarity 75.0%; Pred. No. 2.9e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RXVLSYSR 8
 | :|||||

Search completed: August 10, 2006, 23:09:55
Job time : 153 secs

RESULT 15
Q66JN5 BRARE

THIS PAGE BLANK (USE)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 10, 2006, 23:01:01 ; Search time 18.5455 Seconds
(without alignments)
46.693 Million cell updates/sec

Title: US-10-825-603-2

Perfect score: 33

Sequence: 1 RXVSLSYRX 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 80.*
1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	90.9	160	2 H88114	protein F53C3.6 [i
2	30	90.9	863	2 B71343	probable ribosomal
3	29	87.9	196	2 G82622	conserved hypotet
4	29	87.9	940	2 S49087	lactoferrin bindin
5	28	84.8	24	2 A33262	heparin-binding gr
6	28	84.8	89	2 I53416	interleukin-8 homo
7	28	84.8	89	2 A53497	pre-B-cell growth-
8	28	84.8	93	2 G01540	cytokine SDF-1-bet
9	28	84.8	93	2 I81182	cytokine - mouse
10	28	84.8	172	2 T10891	hemolysin-coregula
11	28	84.8	218	2 B81150	bacteriocin resist
12	28	84.8	218	2 H81871	probable periplasm
13	28	84.8	226	2 F81326	H+-transporting tw
14	28	84.8	226	2 D64623	H+-transporting tw
15	28	84.8	321	2 JCS460	intracellular alka
16	28	84.8	322	2 G83922	intracellular alka
17	28	84.8	380	2 T23875	hypothetical prote
18	28	84.8	435	2 A11017	probable type-I se
19	28	84.8	439	2 T14872	ABC exporter outer
20	28	84.8	468	2 F71422	hypothetical prote
21	28	84.8	596	1 ACRYE	acetylcholinestera
22	28	84.8	599	1 A38868	acetylcholinestera
23	28	84.8	1017	2 D90550	vsaa-like (mycopla
24	28	84.8	93	2 D95074	hypothetical prote
25	27	81.8	160	2 G71122	hypothetical prote
26	27	81.8	201	2 E75567	hypothetical prote
27	27	81.8	287	2 AD3412	aminomethyltransfe
28	27	81.8	385	2 C86909	hypothetical prote
29	27	81.8			

30	27	81.8	385	2	T10003	recF protein - Myc
31	27	81.8	432	2	B86220	protein F22013.31
32	27	81.8	441	2	T00738	hypothetical prote
33	27	81.8	518	2	H64775	probable membrane
34	27	81.8	518	2	F90692	hypothetical prote
35	27	81.8	518	2	B85543	hypothetical prote
36	27	81.8	593	2	T18977	hypothetical prote
37	27	81.8	1086	2	T18294	Ca2+-transporting
38	27	81.8	1423	2	A49206	exo-beta-D-fructos
39	27	81.8	1500	2	T03824	probable immediate
40	27	81.8	1513	2	T44045	hypothetical prote
41	27	81.8	1520	2	T44231	hypothetical prote
42	26	78.8	212	2	AB2611	hypothetical prote
43	26	78.8	212	2	H97392	mca/sah nucleosida
44	26	78.8	214	2	G83488	probable permease
45	26	78.8	266	2	T36341	probable esterase

ALIGNMENTS

RESULT 1

H88114
protein F53C3.6 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C;Accession: H88114
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolo
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/projects/C.el
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; an
A;Accession: H88114
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-160 <STO>
A;Cross-references: UNIPARC:UPI000017A590; GB:chr_II; PIDN:AC67457.1; PID:G3786484; GSP
C;Genetics:
A;Gene: F53C3.6
A;Map position: 2

Query Match 90.9%; Score 30; DB 2; Length 160;
Best Local Similarity 75.0%; Pred. No. 7.6;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RXVSLSYR 8

Db 4 RQVSIYSR 11

RESULT 2

B71343
probable ribosomal protein S1 (rpsA) - syphilis spirochete
C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C;Accession: B71343
R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwi
rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDi
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A;Reference number: A71250; MUID:98332770; PMID:9665876
A;Accession: B71343
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-863 <COL>
A;Cross-references: UNIPROT:083303; UNIPARC:UPI000000D3228; GB:AE001209; GB:AE000520; NI
C;Genetics:
A;Experimental source: strain Nichols
A;Gene: TP0279

Query Match 90.9%; Score 30; DB 2; Length 863;

Best Local Similarity 75.0%; Pred. No. 42;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RXVSLSYR 8
| : |||||
DB 135 RTVALSYR 142

RESULT 3
G82622
conserved hypothetical protein XP1919 [imported] - Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 31-Dec-2004
C:Accession: G82622
R:anonymous; The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MUID:20365717; PMID:10910347
A:Note: for a complete list of authors see reference number A59328 below
A:Accession: G82622
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-196 <SIM>
A:Cross-references: UNIPROT:Q9PC62; UNIPARC:UPI00000C289A; GB:AE004011; GB:AE003849; NID
A:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Bionès, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
ab-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fröh
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tshunako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A:Reference number: A59328
A:Contents: annotation
A:Gene: XF1919
C:Genetics:
C:Superfamily: NAD(P)H-dependent FMN reductase (sulfate starvation-induced protein 4)
Query Match 87.9%; Score 29; DB 2; Length 196;
Best Local Similarity 62.5%; Pred. No. 17;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RXVSLSYR 8
| : |||||
DB 176 RMISISYR 183

RESULT 4
S49087
lactoferrin binding protein - Neisseria meningitidis
C:Species: Neisseria meningitidis
C>Date: 16-Feb-1995 #sequence_revision 12-May-1995 #text_change 09-Jul-2004
C:Accession: S49087
R:Pettersson, A.M.; Klarenbeek, X.Y.Z.; van Deurzen, X.Y.Z.; Poolman, X.Y.Z.; Tommassen,
submitted to the EMBL Data Library, June 1994
A:Description: Molecular characterization of the structural gene for the lacto-ferrin re
A:Reference number: S49087
A:Accession: S49087
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-940 <PET>
A:Cross-references: UNIPROT:Q51187; UNIPARC:UPI0000B941B; EMBL:X79838; NID:g509053; PID
C:Superfamily: ferrichrome-iron receptor; tonB-dependent receptor amino-terminal homolog
F:73-215/Domain: tonB-dependent receptor amino-terminal homolog <TNN>
F:603-940/Domain: tonB-dependent receptor carboxyl-terminal homolog <TNC>
Query Match 87.9%; Score 29; DB 2; Length 940;
Best Local Similarity 75.0%; Pred. No. 82;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RXVSLSYR 8
| : |||||
DB 660 RHLSLSYR 667

RESULT 5
A33262
heparin-binding growth factor A light chain - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 21-Feb-1990 #sequence_revision 21-Feb-1990 #text_change 09-Jul-2004
C:Accession: A33262
R:Zarnegar, R.; Muga, S.; Enghild, J.; Michalopoulos, G.
Biochem. Biophys. Res. Commun. 163, 1370-1376, 1989
A:Title: NH-2-terminal amino acid sequence of rabbit hepatopoietin A, a heparin-binding
A:Reference number: A33262; MUID:89392048; PMID:2528955
A:Accession: A33262
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-24 <ZAR>
A:Cross-references: UNIPROT:P13571; UNIPARC:UPI000012CB72
A:Superfamily: hepatocyte growth factor/macrophage stimulating protein 1; kringle homolo
C:Keywords: growth factor; heparin binding; kringle
Query Match 84.8%; Score 28; DB 2; Length 24;
Best Local Similarity 75.0%; Pred. No. 3.5;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RXVSLSYR 8
| : |||||
DB 13 RMVSLKYR 20

RESULT 6
I53416
interleukin-8 homolog - mouse
C:Species: Mus sp. (mouse)
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C:Accession: I53416
R:Jiang, W.; Zhou, P.; Kahn, S.M.; Tomita, N.; Johnson, M.D.; Weinstein, I.B.
Exp. Cell Res. 215, 284-293, 1994
A:Title: Molecular cloning of TPARI, a gene whose expression is repressed by the tumor p
A:Reference number: I53416; MUID:95073497; PMID:7982471
A:Accession: I53416
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-89 <RES>
A:Cross-references: UNIPARC:UPI00000018A3; GB:S74318; NID:g786393; PIDN:AAB32650.1; PID:
C:Genetics:
A:Gene: TPARI
C:Superfamily: beta-thromboglobulin
Query Match 84.8%; Score 28; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 VLSLYR 8
| : |||||
DB 24 VLSLYR 29

RESULT 7
A53497
pre-B-cell growth-stimulating factor precursor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 09-Jul-2004
C:Accession: A53497; I59582
R:Nagasawa, T.; Kikutani, H.; Kishimoto, T.
Proc. Natl. Acad. Sci. U.S.A. 91, 2305-2309, 1994
A:Title: Molecular cloning and structure of a pre-B-cell growth-stimulating factor.
A:Reference number: A53497; MUID:94181581; PMID:8134392
A:Accession: A53497

A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-89 <NAG>
A;Cross-references: UNIPROT:P40224; UNIPARC:UPI00000018A3; GB:D21072; NID:G413905; PIDN:
R;Tashiro, K.; Tada, H.; Heilker, R.; Shirozu, M.; Nakano, T.; Honjo, T.
Science 261, 600-603, 1993
A;Title: Signal sequence trap: a cloning strategy for secreted proteins and type I membe
A;Reference number: I59582; MUID:93342488; PMID:8342023
A;Accession: I59582
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-89 <RES>
A;Cross-references: UNIPARC:UPI00000018A3; GB:L12029; NID:G393179; PIDN:AAA40100.1; PID:
C;Genetics:
A;Gene: SDF-1-alpha
C;Superfamily: beta-thromboglobulin
C;Keywords: cytokine

Query Match 84.8%; Score 28; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 VLSYR 8
Db 24 VLSYR 29
|||||

RESULT 8
G01540
cytokine SDF-1-beta - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
C;Accession: G01540
R;Spocilla, L.D.
submitted to the EMBL Data Library, October 1994
A;Reference number: G07697
A;Accession: G01540
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-93 <SPO>
A;Cross-references: UNIPROT:P48061; UNIPARC:UPI000003092F; EMBL:U16752; NID:gl272194; PI
C;Superfamily: beta-thromboglobulin

Query Match 84.8%; Score 28; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 VLSYR 8
Db 24 VLSYR 29
|||||

RESULT 9
I81182
cytokine - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C;Accession: I81182
R;Tashiro, K.; Tada, H.; Heilker, R.; Shirozu, M.; Nakano, T.; Honjo, T.
Science 261, 600-603, 1993
A;Title: Signal sequence trap: a cloning strategy for secreted proteins and type I membe
A;Reference number: I59582; MUID:93342488; PMID:8342023
A;Accession: I81182
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-93 <RES>
A;Cross-references: UNIPROT:P40224; UNIPARC:UPI000002A125; GB:L12030; NID:G393181; PIDN:
C;Genetics:
A;Gene: SDF-1-beta
C;Superfamily: beta-thromboglobulin

Query Match 84.8%; Score 28; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 14;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 VLSYR 8
Db 24 VLSYR 29
|||||

RESULT 10
T10891
hemolysin-coregulated protein Hcp VC1415 VCA0017 [similarity] - Vibrio cholerae (strain
C;Species: Vibrio cholerae
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T10891; C82202; E82511
R;Williams, S.G.; Varcoe, L.T.; Attridge, S.R.; Manning, P.A.
Infect. Immun. 64, 283-289, 1996
A;Title: Vibrio cholerae Hcp, a secreted protein coregulated with HlyA.
A;Reference number: Z17200; MUID:96110945; PMID:8557353
A;Accession: T10891
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-172 <WIL>
A;Cross-references: UNIPROT:P72350; UNIPARC:UPI00000D40CC; EMBL:S81006; NID:G1488370; P
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bae, S.; Qin, H.; Dragoi, I.; Sellers,
l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: C82202
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-172 <HEI>
A;Cross-references: UNIPARC:UPI00000D40CC; GB:AE004220; GB:AE003852; NID:G9655910; PIDN
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
A;Accession: E82511
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-172 <HE2>
A;Cross-references: UNIPARC:UPI00000D40CC; GB:AE004345; GB:AE003853; NID:G9657390; PIDN
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics: <GEN1>
A;Gene: hcpB
A;Note: the hcpA and hcpB proteins are identical
C;Genetics: <GEN2>
A;Gene: VC1415
A;Map position: 1
C;Genetics: <GEN3>
A;Gene: VCA0017
A;Map position: 2
C;Superfamily: Vibrio cholerae hemolysin-coregulated protein

Query Match 84.8%; Score 28; DB 2; Length 172;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 VLSYR 8
Db 144 VLSYR 149
|||||

RESULT 11
B81150
bacteriocin resistance protein, probable NMB0855 [imported] - Neisseria meningitidis (s.
C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: B81150
R;Tetzelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; V
A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A;Reference number: A81000; MUID:20175755; PMID:10710307

A:Accession: B81150
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-218 <TET>
 A:Cross-references: UNIPROT:Q9JZX8; UNIPARC:UPI00000C45AB; GB:AE002439; GB:AE002098; NID
 A:Experimental source: serogroup B, strain MCS8
 C:Genetics:
 A:Gene: NMB0855

Query Match 84.8%; Score 28; DB 2; Length 218;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 VLSYSR 8
 |||||
 Db 15 VLSYSR 20
 |||||

RESULT 12

H81871
 probable periplasmic protein NMA1066 [imported] - Neisseria meningitidis (strain Z2491 e
 C:Species: Neisseria meningitidis
 C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
 C:Accession: H81871
 R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
 ; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
 Nature 404, 502-506, 2000
 A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
 A:Reference number: A81775; MUID:20222556; PMID:10761919
 A:Accession: H81871
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-218 <PAR>
 A:Cross-references: UNIPROT:Q9JUZ8; UNIPARC:UPI00000C4AED; GB:AL162755; GB:AL157959; NID
 A:Experimental source: serogroup A, strain Z2491
 C:Genetics:
 A:Gene: NMA1066

Query Match 84.8%; Score 28; DB 2; Length 218;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 VLSYSR 8
 |||||
 Db 15 VLSYSR 20
 |||||

RESULT 13

F81326
 H+-transporting two-sector ATPase (EC 3.6.3.14) protein 6 Cj1204c [similarity] - Campylo
 C:Species: Campylobacter jejuni
 C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 31-Dec-2004
 C:Accession: F81326
 R:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling
 C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrell
 Nature 403, 665-668, 2000
 A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp
 A:Reference number: A81250; MUID:20150912; PMID:10698204
 A:Accession: F81326
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-226 <PAR>
 A:Cross-references: UNIPROT:Q9PN91; UNIPARC:UPI00000D4022; GB:AL139077; GB:AL111168; NID
 A:Experimental source: serotype O2, strain NCTC 11168
 C:Genetics:
 A:Gene: atpB; Cj1204c
 C:Superfamily: H(+)-transporting ATP synthase protein 6
 C:Keywords: ATP biosynthesis; hydrolase; membrane-associated complex

Query Match 84.8%; Score 28; DB 2; Length 226;
 Best Local Similarity 75.0%; Pred. No. 34;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 VLSYSR 8
 |||||
 Db 15 VLSYSR 20
 |||||

Qy 1 RXVLSYSR 8
 |||||
 Db 159 RVVLSFR 166
 |||||

RESULT 14

D64623
 H+-transporting two-sector ATPase (EC 3.6.3.14) chain a - Helicobacter pylori (strain 26
 C:Species: Helicobacter pylori
 C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 31-Dec-2004
 C:Accession: D64623
 R:Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.
 Peterson, S.; Lotius, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne
 son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, I
 Nature 388, 539-547, 1997
 A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C
 A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
 A:Reference number: A64520; MUID:97394467; PMID:9252185
 A:Accession: D64623
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA
 A:Residues: 1-226 <TOM>
 A:Cross-references: UNIPROT:P56085; UNIPARC:UPI000012630D; GB:AE000594; GB:AE000511; NID
 C:Superfamily: H(+)-transporting ATP synthase protein 6
 C:Keywords: ATP biosynthesis; hydrolase; membrane-associated complex

Query Match 84.8%; Score 28; DB 2; Length 226;
 Best Local Similarity 75.0%; Pred. No. 34;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RXVLSYSR 8
 |||||
 Db 159 RVVLSFR 166
 |||||

RESULT 15

G71890
 H+-transporting two-sector ATPase (EC 3.6.3.14) chain a - Helicobacter pylori (strain J9
 C:Species: Helicobacter pylori
 A:Variety: strain J99
 C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 31-Dec-2004
 C:Accession: G71890
 R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
 ; Ives, C.; Gibson, R.; Merberg, D.; Miller, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
 Nature 397, 176-180, 1999
 A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
 A:Reference number: A71800; MUID:99120557; PMID:9923682
 A:Accession: G71890
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-226 <ARN>
 A:Cross-references: UNIPROT:Q9ZL15; UNIPARC:UPI000012630C; GB:AE001507; GB:AE001439; NID
 A:Experimental source: strain J99
 C:Genetics:
 A:Gene: atpB
 C:Superfamily: H(+)-transporting ATP synthase protein 6
 C:Keywords: ATP biosynthesis; hydrolase; membrane-associated complex

Query Match 84.8%; Score 28; DB 2; Length 226;
 Best Local Similarity 75.0%; Pred. No. 34;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RXVLSYSR 8
 |||||
 Db 159 RVVLSFR 166
 |||||

Search completed: August 10, 2006, 23:11:07
 Job time : 20.5455 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 10, 2006, 23:01:01 ; Search time 18.5455 Seconds
(without alignments)
46.693 Million cell updates/sec

Title: US-10-825-603-5

Perfect score: 43

Sequence: 1 RSVLSYRF 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 80.*

1: Pirl.*

2: Pirl.*

3: Pirl.*

4: Pirl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	81.4	468	2 F71422	hypothetical prote
2	32	74.4	219	2 S56899	probable membrane
3	32	74.4	257	2 B64352	hypothetical prote
4	32	74.4	323	2 B72224	conserved hypotet
5	32	74.4	338	2 T43440	hypothetical prote
6	32	74.4	380	2 T29875	hypothetical prote
7	32	74.4	516	2 T00791	purple acid phosph
8	32	74.4	682	2 B70121	hypothetical prote
9	31	72.1	160	2 H88114	protein F53C3.6 [i
10	31	72.1	194	2 A10489	conserved hypotet
11	31	72.1	201	2 E75567	hypothetical prote
12	31	72.1	238	2 I40703	outer membrane pro
13	31	72.1	238	2 I62385	outer membrane pro
14	31	72.1	240	2 I62394	outer membrane pro
15	31	72.1	241	2 I62387	outer membrane pro
16	31	72.1	241	2 I62391	outer membrane pro
17	31	72.1	243	2 I62386	outer membrane pro
18	31	72.1	244	2 I62393	outer membrane pro
19	31	72.1	244	2 I62389	outer membrane pro
20	31	72.1	315	2 E83874	nickel ABC transpo
21	31	72.1	337	2 E95871	probable oxidoredu
22	31	72.1	350	1 MMEBAT	outer membrane pro
23	31	72.1	350	2 A10526	outer membrane pro
24	31	72.1	350	2 S07222	outer membrane pro
25	31	72.1	353	2 AD0175	probable outer mem
26	31	72.1	432	2 B86220	protein F22013.31
27	31	72.1	441	2 T00738	hypothetical prote
28	31	72.1	484	2 A58663	catalase [EC 1.11.
29	31	72.1	544	2 S73388	probable phenylala

RESULT 1

F71422

C:Species: Arabidopsis thaliana

A:Variety: columbia

C:Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 09-Jul-2004

C:Accession: F71422

R:Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dir

P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzensegger, T.; Pohl, T.M.; Terryn, N.; Gie

avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B.

Nature 391, 485-488, 1998

A:Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenech

erhoff, A.; Moeres, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; An

C.; Chalwatzis, N.

A:Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis tha

A:Reference number: A71400; MUID:98121113; PMID:9461215

A:Accession: F71422

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-468 <BEV>

A:Cross-references: UNIPROT:O23425; UNIPARC:UPI00000A66PB; GB:257339; NID:g2244901; PID

C:Genetics:

A:Map position: 4COP9-4G3845

Query Match 81.4%; Score 35; DB 2; Length 468;

Best Local Similarity 87.5%; Pred. No. 10;

Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SVLSYRF 9

DB 174 TVLSYRF 181

RESULT 2

S56899

probable membrane protein YJL118w - yeast (Saccharomyces cerevisiae)

N/Alternate names: hypothetical protein J0742

C:Species: Saccharomyces cerevisiae

C:Date: 08-Jul-1995 #sequence_revision 08-Sep-1995 #text_change 09-Jul-2004

C:Accession: S56899

R:Czipluch, C.; Kordes, E.; Pujol, A.; Jauniaux, J.C.

submitted to the Protein Sequence Database, September 1995

A:Reference number: S56891

A:Accession: S56899

A:Molecule type: DNA

A:Residues: 1-219 <CZI>

A:Cross-references: UNIPROT:P47022; UNIPARC:UPI000013B5E7; EMBL:Z49394; NID:g1008309; P

C:Genetics:

A:Gene: MIPS:YJL118w

A:Cross-references: SGD:S0003654

A:Map position: 10L

C:Superfamily: Saccharomyces cerevisiae probable membrane protein YJL118w

arginyl-tRNA synth
probable TonB-depe
probable ribosomal
serine/threonine k
vacuolar protein s
hypothetical 13.2K
hypothetical 13.2K
transposase sl158
probable permease
bidirectional hydr
hypothetical prote
hypothetical 35.5K
probable succinyl-
hypothetical prote
protein T2SN20.2 l
protein translocas
probable membrane

ALIGNMENTS

RESULT 1

F71422

C:Species: Arabidopsis thaliana

A:Variety: columbia

C:Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 09-Jul-2004

C:Accession: F71422

R:Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dir

P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzensegger, T.; Pohl, T.M.; Terryn, N.; Gie

avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B.

Nature 391, 485-488, 1998

A:Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenech

erhoff, A.; Moeres, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; An

C.; Chalwatzis, N.

A:Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis tha

A:Reference number: A71400; MUID:98121113; PMID:9461215

A:Accession: F71422

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-468 <BEV>

A:Cross-references: UNIPROT:O23425; UNIPARC:UPI00000A66PB; GB:257339; NID:g2244901; PID

C:Genetics:

A:Map position: 4COP9-4G3845

Query Match 81.4%; Score 35; DB 2; Length 468;

Best Local Similarity 87.5%; Pred. No. 10;

Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SVLSYRF 9

DB 174 TVLSYRF 181

RESULT 2

S56899

probable membrane protein YJL118w - yeast (Saccharomyces cerevisiae)

N/Alternate names: hypothetical protein J0742

C:Species: Saccharomyces cerevisiae

C:Date: 08-Jul-1995 #sequence_revision 08-Sep-1995 #text_change 09-Jul-2004

C:Accession: S56899

R:Czipluch, C.; Kordes, E.; Pujol, A.; Jauniaux, J.C.

submitted to the Protein Sequence Database, September 1995

A:Reference number: S56891

A:Accession: S56899

A:Molecule type: DNA

A:Residues: 1-219 <CZI>

A:Cross-references: UNIPROT:P47022; UNIPARC:UPI000013B5E7; EMBL:Z49394; NID:g1008309; P

C:Genetics:

A:Gene: MIPS:YJL118w

A:Cross-references: SGD:S0003654

A:Map position: 10L

C:Superfamily: Saccharomyces cerevisiae probable membrane protein YJL118w

C;Keywords: transmembrane protein

```

Query Match          74.4%; Score 32; DB 2; Length 219;
Best Local Similarity 77.8%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RSVLSLYRF 9
    |||||
Db 58 RSVSTVYRF 66

RESULT 3
B64352
hypothetical protein MJ0418 - Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: B64352
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C
A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A;Reference number: A64300; MUID:96337999; PMID:8688087
A;Accession: B64352
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-257 <BU>
A;Cross-references: UNIPROT:Q57861; UNIPARC:UPI000013979E; GB:U67494; GB:L77117; NID:g15
C;Genetics:
A;Map position: FOR376618-377391
A;Start codon: GTG

Query Match          74.4%; Score 32; DB 2; Length 257;
Best Local Similarity 75.0%; Pred. No. 24;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SVLSLYRF 9
    |||||
Db 22 SVSLAYKF 29

RESULT 4
B72224
conserved hypothetical protein - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: B72224
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
C.M.
Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: B72224
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-323 <ARN>
A;Cross-references: UNIPROT:Q9X1Z0; UNIPARC:UPI000000C123B; GB:AE001808; GB:AE000512; NID
A;Experimental source: strain MSB8
C;Genetics:
A;Gene: TMI660

Query Match          74.4%; Score 32; DB 2; Length 323;
Best Local Similarity 66.7%; Pred. No. 31;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RSVLSLYRF 9
    |||||
Db 262 KSVSAAYRF 270

RESULT 5

```

```

T43440
hypothetical protein DKFZp434K0514.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C;Accession: T43440
R;Koehrer, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, December 1999
A;Reference number: Z22514
A;Accession: T43440
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-338 <AAA>
A;Cross-references: UNIPROT:Q8TBZ3; UNIPARC:UPI000016AC8F; EMBL:AL133558
A;Experimental source: adult testis; clone DKFZp434K0514
C;Genetics:
A;Note: DKFZp434K0514.1

Query Match          74.4%; Score 32; DB 2; Length 338;
Best Local Similarity 66.7%; Pred. No. 32;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RSVLSLYRF 9
    |||||
Db 130 RPSVSTVYRF 138

RESULT 6
T29875
hypothetical protein F32B5.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Dec-2004
C;Accession: T29875
R;Ledwith, J.; Graves, T.; Biewald, T.
submitted to the EMBL Data Library, May 1997
A;Description: The sequence of C. elegans cosmid F32B5.
A;Reference number: Z20702
A;Accession: T29875
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-380 <LED>
A;Cross-references: UNIPROT:O01853; UNIPARC:UPI00000783FE; EMBL:AF003148; PIDN:AAB54207.
A;Experimental source: strain Bristol N2; clone F32B5
C;Genetics:
A;Gene: CESP:F32B5.2
A;Map position: 1
A;Introns: 47/3; 99/2; 195/3; 227/1; 264/2; 333/3

Query Match          74.4%; Score 32; DB 2; Length 380;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SVLSLYR 8
    |||||
Db 287 SVLSLYR 293

RESULT 7
T00791
purple acid phosphatase-related protein At2g32770 [similarity] - Arabidopsis thaliana
N;Alternate names: hypothetical protein F24L7.9
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 05-Oct-2004
C;Accession: T00791; C84737
R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul
submitted to the EMBL Data Library, February 1998
A;Description: Arabidopsis thaliana chromosome II BAC F24L7 genomic sequence.
A;Reference number: Z14204
A;Accession: T00791
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-516 <ROU>
A;Cross-references: UNIPROT:O48840; UNIPARC:UPI00000485E3; EMBL:AC003974; NID:g2914688;
A;Experimental source: cultivar Columbia

```


R.; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Unayam, L.; Taiton, L.; euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999

A>Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Accession: C84737
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-516 <STO>
A:Cross-references: UNIPARC:UPI00000485E3; GB:AE002093; NID:g2914696; PIDN:AAC04486.1; G
C:Genetics:
A:Map position: 2
A:Gene: At2g32770; F24L7.9
A:Introns: 90/1; 279/2; 324/1; 387/3; 478/3
C:Superfamily: Purple acid phosphatase, kidney bean type; phosphoesterase core homology

Query Match 74.4%; Score 32; DB 2; Length 516;
Best Local Similarity 87.5%; Pred. No. 51;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 SVLSYRF 9
|||||
Db 73 SVLSYSF 80

RESULT 8
B70121
hypothetical protein BB0170 - Lyme disease spirochete
C:Species: *Borrelia burgdorferi* (Lyme disease spirochete)
C:Date: 13-Feb-1998 #sequence_revision 13-feb-1998 #text_change 09-Jul-2004
C:Accession: B70121
R; Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White
son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,
; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A:Authors: Smith, H.O.; Venter, J.C.
A>Title: Genomic sequence of a Lyme disease spirochaete, *Borrelia burgdorferi*.
A:Reference number: A70100; MUID:98065943; PMID:9403685
A:Accession: B70121
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-682 <KLE>
A:Cross-references: UNIPROT:O51182; UNIPARC:UPI0000057395; GB:AE001128; GB:AE000783; NID
A:Experimental source: strain B31
C:Superfamily: *Borrelia burgdorferi* hypothetical protein BB0170

Query Match 74.4%; Score 32; DB 2; Length 682;
Best Local Similarity 85.7%; Pred. No. 69;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 VLSYRF 9
|||
Db 576 VLSYRF 582

RESULT 9
H88114
protein F53C3.6 [imported] - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C:Accession: H88114
R; anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A>Title: Genome sequence of the nematode *C. elegans*: a platform for investigating biolog
A:Reference number: A75000; MUID:99069613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_ele
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A:Accession: H88114
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-160 <STO>
A:Cross-references: UNIPARC:UPI000017AS90; GB:chr_II; PIDN:AC67457.1; PID:g3786484; GSPD

C:Genetics:
A:Gene: F53C3.6
A:Map position: 2

Query Match 72.1%; Score 31; DB 2; Length 160;
Best Local Similarity 75.0%; Pred. No. 24;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RSVLSYR 8
|||
Db 4 RQVSISYR 11

RESULT 10
AI0489
conserved hypothetical protein (partial) YPO4026 [imported] - *Yersinia pestis* (strain C;
C:Species: *Yersinia pestis*
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 04-Aug-2003
C:Accession: AI0489
R; Farkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A>Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AI0489
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-194 <KUR>
A:Cross-references: UNIPARC:UPI00000CDAD3; GB:AL590842; PIDN:CAC93485.1; PID:g15981930;
C:Genetics:
A:Gene: YPO4026
C:Superfamily: virulence protein, RhuM type

Query Match 72.1%; Score 31; DB 2; Length 194;
Best Local Similarity 85.7%; Pred. No. 30;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 VLSYRF 9
|||
Db 11 VLSYKF 17

RESULT 11
E75567
hypothetical protein - *Deinococcus radiodurans* (strain R1)
C:Species: *Deinococcus radiodurans*
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: E75567
R; White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; M
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A>Title: Genome sequence of the radioreistant bacterium *Deinococcus radiodurans* R1.
A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: E75567
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-201 <WHI>
A:Cross-references: UNIPROT:Q9RYB3; UNIPARC:UPI00000C16A8; GB:AE001867; GB:AE000513; NI
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR0037
A:Map position: 1

Query Match 72.1%; Score 31; DB 2; Length 201;
Best Local Similarity 87.5%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RSVLSYR 8
|||
Db 112 RSPSLSYR 119

RESULT 12

I40703
outer membrane protein A - Citrobacter freundii (fragment)
N:Alternate names: outer membrane protein II
C:Species: Citrobacter freundii
C:Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C:Accession: I40703
R:Lawrence, J.G.; Ochman, H.; Hartl, D.L.
J. Gen. Microbiol. 137, 1911-1921, 1991
A:Title: Molecular and evolutionary relationships among enteric bacteria.
A:Reference number: I40701; MUID:92065252; PMID:1955870
A:Accession: I40703
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-238 <RES>
A:Cross-references: UNIPROT:P24016; UNIPARC:UPI0000130CEF; GB:M63354; NID:g144441; PIDN:
C:Genetics:
A:Gene: ompA
C:Superfamily: outer membrane protein A
C:Keywords: membrane protein
F:99-109/Region: alanine/proline-rich

Query Match 72.1%; Score 31; DB 2; Length 238;
Best Local Similarity 75.0%; Pred. No. 37;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SVSLSYRF 9
||:||||
Db 85 SVGVSYRF 92

RESULT 13

I62385
outer membrane protein ompA - Escherichia vulneris (fragment)
N:Alternate names: outer membrane protein II
C:Species: Escherichia vulneris
C:Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 09-Jul-2004
C:Accession: I62385
R:Lawrence, J.G.; Ochman, H.; Hartl, D.L.
J. Gen. Microbiol. 137, 1911-1921, 1991
A:Title: Molecular and evolutionary relationships among enteric bacteria.
A:Reference number: I40701; MUID:92065252; PMID:1955870
A:Accession: I62385
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-238 <RES>
A:Cross-references: UNIPROT:Q99114; UNIPARC:UPI00000B0580; GB:M63348; NID:g146984; PIDN:
C:Genetics:
A:Gene: ompA
C:Superfamily: outer membrane protein A
C:Keywords: membrane protein
F:98-109/Region: alanine/proline-rich

Query Match 72.1%; Score 31; DB 2; Length 238;
Best Local Similarity 75.0%; Pred. No. 37;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SVSLSYRF 9
||:||||
Db 85 SVGVSYRF 92

RESULT 14

I62394
outer membrane protein ompA - Escherichia blattae (ATCC 33430) (fragment)
N:Alternate names: outer membrane protein II
C:Species: Escherichia blattae
A:Variety: ATCC 33430
C:Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 09-Jul-2004
C:Accession: I62394
R:Lawrence, J.G.; Ochman, H.; Hartl, D.L.
J. Gen. Microbiol. 137, 1911-1921, 1991

A:Title: Molecular and evolutionary relationships among enteric bacteria.
A:Reference number: I40701; MUID:92065252; PMID:1955870
A:Accession: I62394
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-240 <RES>
A:Cross-references: UNIPROT:Q99124; UNIPARC:UPI000016EC3C; GB:M63345; NID:g147002; PIDN:
A:Experimental source: ATCC 33430
C:Genetics:
A:Gene: ompA
C:Superfamily: outer membrane protein A
C:Keywords: membrane protein
F:100-111/Region: alanine/proline-rich

Query Match 72.1%; Score 31; DB 2; Length 240;
Best Local Similarity 75.0%; Pred. No. 37;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SVSLSYRF 9
||:||||
Db 88 SVGVSYRF 95

RESULT 15

I62387
outer membrane protein A - Escherichia blattae (fragment)
N:Alternate names: outer membrane protein II
C:Species: Escherichia blattae
C:Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 09-Jul-2004
C:Accession: I62387
R:Lawrence, J.G.; Ochman, H.; Hartl, D.L.
J. Gen. Microbiol. 137, 1911-1921, 1991
A:Title: Molecular and evolutionary relationships among enteric bacteria.
A:Reference number: I40701; MUID:92065252; PMID:1955870
A:Accession: I62387
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-241 <RES>
A:Cross-references: UNIPROT:Q99124; UNIPARC:UPI0000130CF2; GB:M63343; NID:g146988; PIDN:
C:Genetics:
A:Gene: ompA
C:Superfamily: outer membrane protein A
C:Keywords: membrane protein
F:101-112/Region: alanine/proline-rich

Query Match 72.1%; Score 31; DB 2; Length 241;
Best Local Similarity 75.0%; Pred. No. 38;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SVSLSYRF 9
||:||||
Db 88 SVGVSYRF 95

Search completed: August 10, 2006, 23:11:09
Job time : 20.5455 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 10, 2006, 22:52:41 ; Search time 120.273 Seconds
(without alignments)
34.213 Million cell updates/sec

Title: US-10-825-603-1

Perfect score: 43

Sequence: 1 RVSLSYRF 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq 8:*

- 1: Geneseq1980s:*
- 2: Geneseq1990s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001s:*
- 5: Geneseq2002s:*
- 6: Geneseq2003as:*
- 7: Geneseq2003bs:*
- 8: Geneseq2004s:*
- 9: Geneseq2005s:*
- 10: Geneseq2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43	100.0	9	ADU18130	ADU18130 Immune ce
2	43	100.0	9	ADU18134	ADU18134 Immune ce
3	37	86.0	1362	10 AEF31834	Aef31834 Human cor
4	35	81.4	13	2 AAY08435	Aay08435 CXCR-4 re
5	35	81.4	27	9 ADY76935	Ady76935 Chemokine
6	35	81.4	27	9 ADY77047	Ady77047 Chemokine
7	35	81.4	27	9 ADY77011	Ady77011 Chemokine
8	35	81.4	27	9 ADY76971	Ady76971 Chemokine
9	35	81.4	31	9 ADY77010	Ady77010 Chemokine
10	35	81.4	31	9 ADY77046	Ady77046 Chemokine
11	35	81.4	31	9 ADY76934	Ady76934 Chemokine
12	35	81.4	31	9 ADY76970	Ady76970 Chemokine
13	34	79.1	26	9 ADY76973	Ady76973 Chemokine
14	34	79.1	26	9 ADY77013	Ady77013 Chemokine
15	34	79.1	26	9 ADY77049	Ady77049 Chemokine
16	34	79.1	26	9 ADY76937	Ady76937 Chemokine
17	34	79.1	30	9 ADY77012	Ady77012 Chemokine
18	34	79.1	30	9 ADY77048	Ady77048 Chemokine
19	34	79.1	30	9 ADY76972	Ady76972 Chemokine
20	34	79.1	30	9 ADY76936	Ady76936 Chemokine
21	34	79.1	559	3 AAY91971	Aay91971 PMWav-2 R
22	33	76.7	9	8 ADU18131	ADU18131 Immune ce
23	32	74.4	13	2 AAY08436	Aay08436 CXCR-4 re

24	32	74.4	27	9	ADY76959	Ady76959 Chemokine
25	32	74.4	27	9	ADY76965	Ady76965 Chemokine
26	32	74.4	27	9	ADY77041	Ady77041 Chemokine
27	32	74.4	27	9	ADY77035	Ady77035 Chemokine
28	32	74.4	31	9	ADY76958	Ady76958 Chemokine
29	32	74.4	31	9	ADY76964	Ady76964 Chemokine
30	32	74.4	31	9	ADY77034	Ady77034 Chemokine
31	32	74.4	31	9	ADY77040	Ady77040 Chemokine
32	32	74.4	143	3	AAB38270	Aab38270 Human sec
33	32	74.4	143	3	AAB38268	Aab38268 Human sec
34	32	74.4	182	3	AAB38218	Aab38218 Human sec
35	32	74.4	271	8	ABO60242	AbO60242 Human gen
36	32	74.4	286	4	AAM41880	Aam41880 Human pol
37	32	74.4	300	5	ABP41214	Abp41214 Human ova
38	32	74.4	312	4	AAM40094	Aam40094 Human pol
39	32	74.4	321	4	ADM19825	Adm19825 Protein e
40	32	74.4	396	4	AAG65160	Ag65160 Human myo
41	32	74.4	396	6	ADA54924	Ada54924 Human pro
42	32	74.4	409	8	ADT56544	Adt56544 Plant pol
43	32	74.4	445	7	ADB64055	Adb64055 Human pro
44	32	74.4	516	5	ABB91981	Abb91981 Herbicide
45	32	74.4	557	7	ADK68448	Adk68448 Human myo

ALIGNMENTS

RESULT 1

ADU18130

ID ADU18130 standard; peptide; 9 AA.

AC ADU18130;

XX

DT 27-JAN-2005 (first entry)

XX

DE Immune cell potentiating factor peptide #1.

XX

KW immunostimulant; cytostatic; antimicrobial; antibacterial; virucide;
KW antiparasitic; antitubercular; tuberculosis; immune modulation;
KW bacterial infection; viral infection; parasitic infection; cancer;
KW neoplasia; bioterrorism; surgery; post-operative infection;
KW vaccine adjuvant; immune cell potentiating factor.

OS Capra hircus.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 2 /note= "conjugated to fatty acid on the side chain"

FT Modified-site 9

FT /note= "conjugated to fatty acid groups on the side chain and the C-terminus"

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

CC The invention relates to an isolated peptide having an amino terminus and
 CC a carboxy terminus, selected from four amino acid sequences (A1), (A2),
 CC (A3) and (A4), respectively. (A1: ADU18132), (A2: ADU18131), (A3:
 CC ADU18134) and H2N-Arg-Ser(-O-R1)-Val-Ser-Leu-Ser-Tyr-Arg(-H2N-Phe-O-CH2(-
 CC CH(-CH2-O-R3)-O-R2))-Phe-O-CH2(-CH(-CH2-O-R3)-O-R2) (A4: ADU18130),
 CC respectively where R1-R3 are fatty acid groups (preferably stearic acid,
 CC arachidic acid or arachidonic acid). The peptides can be used for the
 CC treatment or prevention of a mammalian disease or disorder such as,
 CC bacterial, viral or parasitic infections and/or cancer or neoplasia, such
 CC as cholera, dysentery, influenza and tuberculosis, as a prophylactic for
 CC short term protection in a bioterrorism area and other contagion environs
 CC and in patients undergoing major surgery to prevent post-operative
 CC infections, as a vaccine adjuvant to provide long-term protection, and
 CC also useful in adjunctive therapy. The peptides act as immune cell
 CC potentiating factors (ICPF) i.e. immune regulators, exhibit a broad
 CC spectrum of therapeutic efficiency and a wide margin of safety to the
 CC host species with respect to toxic and fetal side effects, as associated
 CC with the prior art ICPFs. The peptides are effective in an amount that
 CC produces a serum concentration of greater than 1 microgram/ml, and are
 CC capable of providing an affordable therapy for serious infectious
 CC diseases. This sequence corresponds to a peptide of the invention
 CC isolated from goat serum.

XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 43; DB 8; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSVSLSYRF 9
 |||||
 Db 1 RSVSLSYRF 9

RESULT 2

ADU18134
 ID ADU18134 standard; peptide; 9 AA.

XX
 AC ADU18134;

XX
 DT 27-JAN-2005 (first entry)

XX
 DE Immune cell potentiating factor peptide #5.

XX immunostimulant; cytostatic; antimicrobial; antibacterial; virucide;
 KW antiparasitic; antitubercular; tuberculostatic; immune modulation;
 KW bacterial infection; viral infection; parasitic infection; cancer;
 KW neoplasia; bioterrorism; surgery; post-operative infection;
 KW vaccine adjuvant; immune cell potentiating factor.

XX
 OS Capra hircus.

OS Synthetic.

XX
 PN WO2004094455-A2.

XX
 PD 04-NOV-2004.

XX
 PF 16-APR-2004; 2004WO-US011896.

XX
 PR 16-APR-2003; 2003US-0463042P.

XX
 PA (GENE-) GENEBACT BIOTECHNOLOGIES INC.

XX
 PI Thacker JD, Fuhrer PJ, Willeford KO;

XX
 DR WPI; 2004-795526/78.

XX
 PT New isolated peptides having an amino terminus and a carboxy terminus
 PT useful for the treatment or prevention of viral and bacterial infections,
 PT comprise amino acids as given in the specification.

XX
 PS Claim 12; SEQ ID NO 5; 55pp; English.

CC The invention relates to an isolated peptide having an amino terminus and
 CC a carboxy terminus, selected from four amino acid sequences (A1), (A2),
 CC (A3) and (A4), respectively. (A1: ADU18132), (A2: ADU18131), (A3:
 CC ADU18134) and H2N-Arg-Ser(-O-R1)-Val-Ser-Leu-Ser-Tyr-Arg(-H2N-Phe-O-CH2(-
 CC CH(-CH2-O-R3)-O-R2))-Phe-O-CH2(-CH(-CH2-O-R3)-O-R2) (A4: ADU18130),
 CC respectively where R1-R3 are fatty acid groups (preferably stearic acid,
 CC arachidic acid or arachidonic acid). The peptides can be used for the
 CC treatment or prevention of a mammalian disease or disorder such as,
 CC bacterial, viral or parasitic infections and/or cancer or neoplasia, such
 CC as cholera, dysentery, influenza and tuberculosis, as a prophylactic for
 CC short term protection in a bioterrorism area and other contagion environs
 CC and in patients undergoing major surgery to prevent post-operative
 CC infections, as a vaccine adjuvant to provide long-term protection, and
 CC also useful in adjunctive therapy. The peptides act as immune cell
 CC potentiating factors (ICPF) i.e. immune regulators, exhibit a broad
 CC spectrum of therapeutic efficiency and a wide margin of safety to the
 CC host species with respect to toxic and fetal side effects, as associated
 CC with the prior art ICPFs. The peptides are effective in an amount that
 CC produces a serum concentration of greater than 1 microgram/ml, and are
 CC capable of providing an affordable therapy for serious infectious
 CC diseases. This sequence corresponds to a peptide of the invention.

XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 43; DB 8; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSVSLSYRF 9
 |||||
 Db 1 RSVSLSYRF 9

RESULT 3

AEF31834
 ID AEF31834 standard; protein; 1362 AA.

XX
 AC AEF31834;

XX
 DT 23-MAR-2006 (first entry)

XX
 DE Human coronavirus HKU1 amino acid sequence SEQ ID NO:420.

XX
 KW virucide; respiratory-gen.; vaccine; respiratory tract infection.

XX
 OS Human coronavirus HKU1.

XX
 PN US2006018923-A1.

XX
 PD 26-JAN-2006.

XX
 PF 21-JUL-2004; 2004US-00895064.

XX
 PR 21-JUL-2004; 2004US-00895064.

XX
 PA (YUEN/) YUEN K Y.

XX
 PA (WOOC/) WOO C Y P.

XX
 PA (LAUK/) LAU K P S.

XX
 PA (CHAN/) CHAN K H.

XX
 PA (POON/) POON L M.

XX
 PA (PEIR/) PEIRIS J S M.

XX
 PA (GUAN/) GUAN Y.

XX
 PI Yuen KY, Woo CYP, Lau KPS, Chan KH, Poon LM, Peiris JSM, Guan Y;

XX
 DR WPI; 2006-109168/11.

XX
 PT New nucleic acid molecule encoding human virus, useful for preventing,
 PT diagnosing, and/or treating infection caused by coronavirus-HKU1, e.g.
 PT respiratory tract infection.

XX
 PS Claim 20; SEQ ID NO 420; 141pp; English.

CC The invention relates to an isolated nucleic acid molecule comprising the
 CC nucleotide sequence of AEF31415 or AEF31417, or its complement, or a
 CC nucleotide sequence encoding the amino acid sequence of AEF31416 or a
 CC complement of the nucleotide sequence. Also described: (1) a vector
 CC comprising the nucleic acid molecule above; (2) a host cell comprising
 CC the vector of (1) or the nucleic acid molecule above operably linked to a
 CC heterologous promoter; (3) producing a polypeptide; (4) preparing a cell
 CC or its progeny, capable of expressing a polypeptide; (5) an isolated
 CC polypeptide encoded by the nucleic acid molecule above; (6) an isolated
 CC antibody or its antigen-binding fragment, which immunospecifically binds
 CC to the polypeptide of (5); (7) detecting the presence of the polypeptide
 CC of (5) in a biological sample; (8) detecting the presence of a first
 CC nucleic acid molecule comprising the nucleotide sequence of AEF31415 or
 CC AEF31417, or its fragment or complement, in a biological sample; (9)
 CC preventing or inhibiting a replication in a host cell of a nucleic acid
 CC molecule comprising the nucleotide sequence of AEF31415 and/or AEF31417,
 CC or its portion or complement; (10) preventing or inhibiting a binding to
 CC a host cell of the polypeptide encoded by a nucleotide sequence of
 CC AEF31415 or AEF31417, or its fragment or complement; (11) detecting the
 CC presence of an antibody in a biological sample that immunospecifically
 CC binds the polypeptides of (5); (12) identifying a subject infected with
 CC human coronavirus HKU1 (CoV-HKU1); and (13) an immunogenic formulation
 CC comprising an immunogenic amount of the polypeptide of (5), or the
 CC nucleic acid molecule comprising the nucleotide sequence of AEF31415 or
 CC AEF31417, its complement or fragment, and a pharmaceutical carrier. The
 CC CoV-HKU1 sequences, composition, vaccine, and method of the invention are
 CC useful for preventing, diagnosing, vaccine, and method of the invention are
 CC CoV-HKU1, e.g. respiratory tract infection. The present sequence
 CC represents a first frame translation amino acid sequence from the CoV-
 CC HKU1 entire genomic DNA sequence of AEF31417, which is used in the
 CC exemplification of the present invention. Note - The sequence listing for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from the USPTO web site. However
 CC all the sequences do appear in either the figures or the disclosure of
 CC the specification.

XX SQ Sequence 1362 AA;

Query Match 86.0%; Score 37; DB 10; Length 1362;
 Best Local Similarity 77.8%; Pred. No. 2.1e+02;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RSVLSLYRF 9
 ||:|||||
 Db 766 RSISASYRF 774

RESULT 4

AA08435
 ID AAY08435 standard; peptide; 13 AA.

XX AC AAY08435;

XX DT 26-JUL-1999 (first entry)

XX DE CXCR-4 receptor binding peptide 20.

XX KW CXCR-4 receptor; antagonist; stroma cell-derived factor-1; SDF-1; HIV-1;
 XX infection; lymphotropic strain; treatment; diagnosis.

XX OS Synthetic.

XX PN DE19734161-A1.

XX PD 01-APR-1999.

XX PF 07-AUG-1997; 97DE-01034161.

XX PR 07-AUG-1997; 97DE-01034161.

XX PA (JERI-) JERINI BIOTOOLS GMBH.

XX PI Schneider-Mergener J, Germeroth L, Heveker N, Alison M;

XX DR

XX WPI; 1999-230182/20.

XX PT Antagonists of stroma cell-derived factor-1, for diagnosis and treatment
 of human immune deficiency virus (HIV) infection.

XX PS Disclosure; Page 17; 20pp; German.

XX CC This invention describes novel antagonists of stroma cell-derived factor-
 1 (SDF-1) which bind to the CXCR-4 receptor, to which SDF-1 normally
 binds, so prevents binding of this receptor to HIV-1, an essential step
 in infection by lymphotropic strains of the virus. The peptides of the
 invention (AAY08416-Y08438) are used to treat or diagnose human immune
 deficiency virus-1 (HIV-1) infection and provide, for the first time, a
 method for antagonizing the interaction between HIV-1 and the CXCR-4
 receptor

XX SQ Sequence 13 AA;

Query Match 81.4%; Score 35; DB 2; Length 13;
 Best Local Similarity 77.8%; Pred. No. 3.4;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RSVLSLYRF 9
 :|||||
 Db 1 KPVSLSYRF 9

RESULT 5

ADV76935
 ID ADY76935 standard; peptide; 27 AA.

XX AC ADY76935;

XX DT 02-JUN-2005 (first entry)

XX DE Chemokine analog peptide #24.

XX KW chemokine; inflammation; antiinflammatory; autoimmune disease;
 XX immunosuppressive; cancer; cytostatic; cardiovascular disease;
 XX cardiovascular-gen.; infection; rheumatoid arthritis; antiarthritic;
 XX antirheumatic; chronic inflammatory bowel disease; antiinflammatory;
 XX gastrointestinal-gen.; multiple sclerosis; neuroprotective; asthma;
 XX antiasthmatic; osteoarthritis; osteopathic; atherosclerosis;
 XX antiatherosclerotic; psoriasis; antipsoriatic; rhinitis; antiallergic;
 XX organ transplant rejection.

XX OS Synthetic.
 XX OS Unidentified.

XX PN US2005059584-A1.

XX PD 17-MAR-2005.

XX PF 16-AUG-2002; 2002US-00222703.

XX PR 16-AUG-2002; 2002US-00222703.

XX PA (MERZ/) MERZOUK A.

XX PA (HABI/) HABI A.

XX PA (WONG/) WONG D.

XX PA (SALA/) SALARI H.

XX PI Merzouk A, Habi A, Wong D, Salari H;

XX WPI; 2005-232172/24.

XX PT Chemokine derived analog compound, useful for treating autoimmune
 diseases, chronic inflammation, cancer, cardiovascular disease, or
 infectious disease.

XX PS Example 17; Fig 17; 104pp; English.

XX XX

CC The invention comprises chemokine derived analog peptides, such as
 CC stromal cell-derived factor-1 (SDF-1) peptides or macrophage inflammatory
 CC protein-1-alpha (MIP-1-alpha) peptides. The chemokine derived analog
 CC peptides of the invention are useful for treating inflammation,
 CC autoimmune diseases, cancer, cardiovascular disease, infections,
 CC rheumatoid arthritis, chronic inflammatory bowel disease, chronic
 CC inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis,
 CC atherosclerosis, psoriasis, rhinitis, and organ transplant rejection. The
 CC present amino acid sequence represents a chemokine analog peptide that
 CC was used in an example of the invention.

XX Sequence 27 AA;

Query Match 81.4%; Score 35; DB 9; Length 27;
 Best Local Similarity 77.8%; Pred. No. 7.4;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RSVSLSYRF 9
 : |||||
 Db 1 KPVSLSYRF 9

RESULT 6
 ADY77047
 ID ADY77047 standard; peptide; 27 AA.

XX AC ADY77047;

XX DT 02-JUN-2005 (first entry)

XX DE Chemokine analog peptide #136.

XX KW chemokine; inflammation; antiinflammatory; autoimmune disease;
 KW immunosuppressive; cancer; cytostatic; cardiovascular disease;
 KW cardiovascular-gen.; infection; rheumatoid arthritis; antiarthritic;
 KW antirheumatic; chronic inflammatory bowel disease; antiinflammatory;
 KW gastrointestinal-gen.; multiple sclerosis; neuroprotective; asthma;
 KW antiasthmatic; osteoarthritis; osteopathic; atherosclerosis;
 KW antiarteriosclerotic; psoriasis; antipsoriatic; rhinitis; antiallergic;
 KW organ transplant rejection.

XX OS Synthetic.

XX OS Unidentified.

XX PN US2005059584-A1.

XX PD 17-MAR-2005.

XX PF 16-AUG-2002; 2002US-00222703.

XX PR 16-AUG-2002; 2002US-00222703.

XX PA (MERZ/) MERZOUK A.

XX PA (HABI/) HABI A.

XX PA (WONG/) WONG D.

XX PA (SALA/) SALARI H.

XX PI Merzouk A, Habi A, Wong D, Salari H;

XX WPI; 2005-232172/24.

XX Chemokine derived analog compound, useful for treating autoimmune
 PT diseases, chronic inflammation, cancer, cardiovascular disease, or
 PT infectious disease.

XX Example 17; Fig 17; 104pp; English.

XX The invention comprises chemokine derived analog peptides, such as
 CC stromal cell-derived factor-1 (SDF-1) peptides or macrophage inflammatory
 CC protein-1-alpha (MIP-1-alpha) peptides. The chemokine derived analog
 CC peptides of the invention are useful for treating inflammation,
 CC autoimmune diseases, cancer, cardiovascular disease, infections,
 CC rheumatoid arthritis, chronic inflammatory bowel disease, chronic

CC inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis,
 CC atherosclerosis, psoriasis, rhinitis, and organ transplant rejection. The
 CC present amino acid sequence represents a chemokine analog peptide that
 CC was used in an example of the invention.

XX Sequence 27 AA;

Query Match 81.4%; Score 35; DB 9; Length 27;
 Best Local Similarity 77.8%; Pred. No. 7.4;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RSVSLSYRF 9
 : |||||
 Db 1 KPVSLSYRF 9

RESULT 7
 ADY77011
 ID ADY77011 standard; peptide; 27 AA.

XX AC ADY77011;

XX DT 02-JUN-2005 (first entry)

XX DE Chemokine analog peptide #100.

XX KW chemokine; inflammation; antiinflammatory; autoimmune disease;
 KW immunosuppressive; cancer; cytostatic; cardiovascular disease;
 KW cardiovascular-gen.; infection; rheumatoid arthritis; antiarthritic;
 KW antirheumatic; chronic inflammatory bowel disease; antiinflammatory;
 KW gastrointestinal-gen.; multiple sclerosis; neuroprotective; asthma;
 KW antiasthmatic; osteoarthritis; osteopathic; atherosclerosis;
 KW antiarteriosclerotic; psoriasis; antipsoriatic; rhinitis; antiallergic;
 KW organ transplant rejection.

XX OS Synthetic.

XX OS Unidentified.

XX PN US2005059584-A1.

XX PD 17-MAR-2005.

XX PF 16-AUG-2002; 2002US-00222703.

XX PR 16-AUG-2002; 2002US-00222703.

XX PA (MERZ/) MERZOUK A.

XX PA (HABI/) HABI A.

XX PA (WONG/) WONG D.

XX PA (SALA/) SALARI H.

XX PI Merzouk A, Habi A, Wong D, Salari H;

XX WPI; 2005-232172/24.

XX Chemokine derived analog compound, useful for treating autoimmune
 PT diseases, chronic inflammation, cancer, cardiovascular disease, or
 PT infectious disease.

XX Example 17; Fig 17; 104pp; English.

XX The invention comprises chemokine derived analog peptides, such as
 CC stromal cell-derived factor-1 (SDF-1) peptides or macrophage inflammatory
 CC protein-1-alpha (MIP-1-alpha) peptides. The chemokine derived analog
 CC peptides of the invention are useful for treating inflammation,
 CC autoimmune diseases, cancer, cardiovascular disease, infections,
 CC rheumatoid arthritis, chronic inflammatory bowel disease, chronic
 CC inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis,
 CC atherosclerosis, psoriasis, rhinitis, and organ transplant rejection. The
 CC present amino acid sequence represents a chemokine analog peptide that
 CC was used in an example of the invention.

XX Sequence 27 AA;

Query Match 81.4%; Score 35; DB 9; Length 27;
 Best Local Similarity 77.8%; Pred. No. 7.4;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RVSLSYRF 9
 DB 1 KPVLSYRF 9

RESULT 8
 ADY76971
 ID ADY76971 standard; peptide; 27 AA.
 XX
 AC ADY76971;
 DT 02-JUN-2005 (first entry)
 DE Chemokine analog peptide #60.
 XX
 KW chemokine; inflammation; antiinflammatory; autoimmune disease;
 KW immunosuppressive; cancer; cytostatic; cardiovascular disease;
 KW cardiovascular-gen.; infection; rheumatoid arthritis; antiarthritic;
 KW antirheumatic; chronic inflammatory bowel disease; antiinflammatory;
 KW gastrointestinal-gen.; multiple sclerosis; neuroprotective; asthma;
 KW antiasthmatic; osteoarthritis; osteopathic; atherosclerosis;
 KW antiarteriosclerotic; psoriasis; antipsoriatic; rhinitis; antiallergic;
 KW organ transplant rejection.
 XX
 OS Synthetic.
 OS Unidentified.
 XX
 PN US2005059584-A1.
 XX
 PD 17-MAR-2005.
 XX
 PF 16-AUG-2002; 2002US-00222703.
 XX
 PR 16-AUG-2002; 2002US-00222703.
 XX
 PA (MERZ/) MERZOUK A.
 PA (HABI/) HABI A.
 PA (WONG/) WONG D.
 PA (SALA/) SALARI H.
 XX
 PI Merzouk A, Habi A, Wong D, Salari H;
 DR WPI; 2005-232172/24.
 XX
 PT Chemokine derived analog compound, useful for treating autoimmune
 PT diseases, chronic inflammation, cancer, cardiovascular disease, or
 PT infectious disease.
 XX
 PS Example 17; Fig 17; 104pp; English.
 XX
 CC The invention comprises chemokine derived analog peptides, such as
 CC stromal cell-derived factor-1 (SDF-1) peptides or macrophage inflammatory
 CC protein-1-alpha (MIP-1-alpha) peptides. The chemokine derived analog
 CC peptides of the invention are useful for treating inflammation,
 CC autoimmune diseases, cancer, cardiovascular disease, infections,
 CC rheumatoid arthritis, chronic inflammatory bowel disease, chronic
 CC inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis,
 CC atherosclerosis, psoriasis, rhinitis, and organ transplant rejection. The
 CC present amino acid sequence represents a chemokine analog peptide that
 CC was used in an example of the invention.
 XX
 SQ Sequence 27 AA;

Query Match 81.4%; Score 35; DB 9; Length 27;
 Best Local Similarity 77.8%; Pred. No. 7.4;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RVSLSYRF 9

Db 1 KPVLSYRF 9

RESULT 9
 ADY77010
 ID ADY77010 standard; peptide; 31 AA.
 XX
 AC ADY77010;
 DT 02-JUN-2005 (first entry)
 DE Chemokine analog peptide #99.
 XX
 KW chemokine; inflammation; antiinflammatory; autoimmune disease;
 KW immunosuppressive; cancer; cytostatic; cardiovascular disease;
 KW cardiovascular-gen.; infection; rheumatoid arthritis; antiarthritic;
 KW antirheumatic; chronic inflammatory bowel disease; antiinflammatory;
 KW gastrointestinal-gen.; multiple sclerosis; neuroprotective; asthma;
 KW antiasthmatic; osteoarthritis; osteopathic; atherosclerosis;
 KW antiarteriosclerotic; psoriasis; antipsoriatic; rhinitis; antiallergic;
 KW organ transplant rejection.
 XX
 OS Synthetic.
 OS Unidentified.
 XX
 PN US2005059584-A1.
 XX
 PD 17-MAR-2005.
 XX
 PF 16-AUG-2002; 2002US-00222703.
 XX
 PR 16-AUG-2002; 2002US-00222703.
 XX
 PA (MERZ/) MERZOUK A.
 PA (HABI/) HABI A.
 PA (WONG/) WONG D.
 PA (SALA/) SALARI H.
 XX
 PI Merzouk A, Habi A, Wong D, Salari H;
 DR WPI; 2005-232172/24.
 XX
 PT Chemokine derived analog compound, useful for treating autoimmune
 PT diseases, chronic inflammation, cancer, cardiovascular disease, or
 PT infectious disease.
 XX
 PS Example 17; Fig 17; 104pp; English.
 XX
 CC The invention comprises chemokine derived analog peptides, such as
 CC stromal cell-derived factor-1 (SDF-1) peptides or macrophage inflammatory
 CC protein-1-alpha (MIP-1-alpha) peptides. The chemokine derived analog
 CC peptides of the invention are useful for treating inflammation,
 CC autoimmune diseases, cancer, cardiovascular disease, infections,
 CC rheumatoid arthritis, chronic inflammatory bowel disease, chronic
 CC inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis,
 CC atherosclerosis, psoriasis, rhinitis, and organ transplant rejection. The
 CC present amino acid sequence represents a chemokine analog peptide that
 CC was used in an example of the invention.
 XX
 SQ Sequence 31 AA;

Query Match 81.4%; Score 35; DB 9; Length 31;
 Best Local Similarity 77.8%; Pred. No. 8.7;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RVSLSYRF 9

RESULT 10
 ADY77046

ID ADY77046 standard; peptide; 31 AA.
 AC ADY77046;
 XX
 DT 02-JUN-2005 (first entry)
 XX
 DE Chemokine analog peptide #135.
 XX
 KW chemokine; inflammation; antiinflammatory; autoimmune disease;
 KW immunosuppressive; cancer; cytostatic; cardiovascular disease;
 KW cardiovascular-gen.; infection; rheumatoid arthritis; antiarthritic;
 KW antirheumatic; chronic inflammatory bowel disease; antiinflammatory;
 KW gastrointestinal-gen.; multiple sclerosis; neuroprotective; asthma;
 KW antiasthmatic; osteoarthritis; osteopathic; atherosclerosis;
 KW antiarteriosclerotic; psoriasis; antipsoriatic; rhinitis; antiallergic;
 KW organ transplant rejection.
 XX
 OS Synthetic.
 OS Unidentified.
 XX
 PN US2005059584-A1.
 XX
 PD 17-MAR-2005.
 XX
 PF 16-AUG-2002; 2002US-00222703.
 XX
 PR 16-AUG-2002; 2002US-00222703.
 XX
 PA (MERZ/) MERZOUK A.
 PA (HABI/) HABI A.
 PA (WONG/) WONG D.
 PA (SALA/) SALARI H.
 XX
 PI Merzouk A, Habi A, Wong D, Salari H;
 XX
 DR WPI; 2005-232172/24.
 XX
 PT Chemokine derived analog compound, useful for treating autoimmune
 PT diseases, chronic inflammation, cancer, cardiovascular disease, or
 PT infectious disease.
 XX
 PS Example 17; Fig 17; 104pp; English.
 XX
 CC The invention comprises chemokine derived analog peptides, such as
 CC stromal cell-derived factor-1 (SDF-1) peptides or macrophage inflammatory
 CC protein-1-alpha (MIP-1-alpha) peptides. The chemokine derived analog
 CC peptides of the invention are useful for treating inflammation,
 CC autoimmune diseases, cancer, cardiovascular disease, infections,
 CC rheumatoid arthritis, chronic inflammatory bowel disease, chronic
 CC inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis,
 CC atherosclerosis, psoriasis, rhinitis, and organ transplant rejection. The
 CC present amino acid sequence represents a chemokine analog peptide that
 CC was used in an example of the invention.
 XX
 SQ Sequence 31 AA;
 Query Match 81.4%; Score 35; DB 9; Length 31;
 Best Local Similarity 77.8%; Pred. No. 8.7; Indels 0; Gaps 0;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 RSVSLSYRF 9
 Db : |||||
 1 KPVSLSYRF 9
 RESULT 11
 ID ADY76934 standard; peptide; 31 AA.
 AC ADY76934;
 XX
 DT 02-JUN-2005 (first entry)
 XX

DE Chemokine analog peptide #23.
 XX
 KW chemokine; inflammation; antiinflammatory; autoimmune disease;
 KW immunosuppressive; cancer; cytostatic; cardiovascular disease;
 KW cardiovascular-gen.; infection; rheumatoid arthritis; antiarthritic;
 KW antirheumatic; chronic inflammatory bowel disease; antiinflammatory;
 KW gastrointestinal-gen.; multiple sclerosis; neuroprotective; asthma;
 KW antiasthmatic; osteoarthritis; osteopathic; atherosclerosis;
 KW antiarteriosclerotic; psoriasis; antipsoriatic; rhinitis; antiallergic;
 KW organ transplant rejection.
 XX
 OS Synthetic.
 OS Unidentified.
 XX
 PN US2005059584-A1.
 XX
 PD 17-MAR-2005.
 XX
 PF 16-AUG-2002; 2002US-00222703.
 XX
 PR 16-AUG-2002; 2002US-00222703.
 XX
 PA (MERZ/) MERZOUK A.
 PA (HABI/) HABI A.
 PA (WONG/) WONG D.
 PA (SALA/) SALARI H.
 XX
 PI Merzouk A, Habi A, Wong D, Salari H;
 XX
 DR WPI; 2005-232172/24.
 XX
 PT Chemokine derived analog compound, useful for treating autoimmune
 PT diseases, chronic inflammation, cancer, cardiovascular disease, or
 PT infectious disease.
 XX
 PS Example 17; Fig 17; 104pp; English.
 XX
 CC The invention comprises chemokine derived analog peptides, such as
 CC stromal cell-derived factor-1 (SDF-1) peptides or macrophage inflammatory
 CC protein-1-alpha (MIP-1-alpha) peptides. The chemokine derived analog
 CC peptides of the invention are useful for treating inflammation,
 CC autoimmune diseases, cancer, cardiovascular disease, infections,
 CC rheumatoid arthritis, chronic inflammatory bowel disease, chronic
 CC inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis,
 CC atherosclerosis, psoriasis, rhinitis, and organ transplant rejection. The
 CC present amino acid sequence represents a chemokine analog peptide that
 CC was used in an example of the invention.
 XX
 SQ Sequence 31 AA;
 Query Match 81.4%; Score 35; DB 9; Length 31;
 Best Local Similarity 77.8%; Pred. No. 8.7; Indels 0; Gaps 0;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 RSVSLSYRF 9
 Db : |||||
 1 KPVSLSYRF 9
 RESULT 12
 ID ADY76970 standard; peptide; 31 AA.
 AC ADY76970;
 XX
 DT 02-JUN-2005 (first entry)
 XX
 DE Chemokine analog peptide #59.
 XX
 KW chemokine; inflammation; antiinflammatory; autoimmune disease;
 KW immunosuppressive; cancer; cytostatic; cardiovascular disease;
 KW cardiovascular-gen.; infection; rheumatoid arthritis; antiarthritic;
 KW antirheumatic; chronic inflammatory bowel disease; antiinflammatory;
 KW

KW gastrointestinal-gen.; multiple sclerosis; neuroprotective; asthma;
 KW antiasthmatic; osteoarthritis; osteopathic; atherosclerosis;
 KW antiarteriosclerotic; psoriasis; antipsoriatic; rhinitis; antiallergic;
 KW organ transplant rejection.

XX Synthetic.
 OS Unidentified.

PN US2005059584-A1.

XX 17-MAR-2005.

PF 16-AUG-2002; 2002US-00222703.

PR 16-AUG-2002; 2002US-00222703.

XX (MERZ/) MERZOUK A.

PA (HABI/) HABI A.

PA (WONG/) WONG D.

PA (SALA/) SALARI H.

XX Merzouk A, Habi A, Wong D, Salari H;

XX WPI; 2005-232172/24.

XX Chemokine derived analog compound, useful for treating autoimmune
 PT diseases, chronic inflammation, cancer, cardiovascular disease, or
 PT infectious disease.

XX Example 17; Fig 17; 104pp; English.

PS The invention comprises chemokine derived analog peptides, such as
 CC stromal cell-derived factor-1 (SDF-1) peptides or macrophage inflammatory
 CC protein-1-alpha (MIP-1-alpha) peptides. The chemokine derived analog
 CC peptides of the invention are useful for treating inflammation,
 CC autoimmune diseases, cancer, cardiovascular disease, infections,
 CC rheumatoid arthritis, chronic inflammatory bowel disease, chronic
 CC inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis,
 CC atherosclerosis, psoriasis, rhinitis, and organ transplant rejection. The
 CC present amino acid sequence represents a chemokine analog peptide that
 CC was used in an example of the invention.

XX Sequence 31 AA;

Query Match 81.4%; Score 35; DB 9; Length 31;

Best Local Similarity 77.8%; Pred. No. 8.7;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RVSLSYRFP 9

DB 1 KPVLSYRFP 9

RESULT 13

ADV76973

ID ADY76973 standard; peptide; 26 AA.

XX AC ADY76973;

XX 02-JUN-2005 (first entry)

XX Chemokine analog peptide #62.

XX Chemokine; inflammation; antiinflammatory; autoimmune disease;

KW immunosuppressive; cancer; cytostatic; cardiovascular disease;

KW cardiovascular-gen.; infection; rheumatoid arthritis; antiarthritic;

KW antirheumatic; chronic inflammatory bowel disease; antiinflammatory;

KW gastrointestinal-gen.; multiple sclerosis; neuroprotective; asthma;

KW antiasthmatic; osteoarthritis; osteopathic; atherosclerosis;

KW antiarteriosclerotic; psoriasis; antipsoriatic; rhinitis; antiallergic;

KW organ transplant rejection.

XX Synthetic.

OS Unidentified.

PN US2005059584-A1.

XX 17-MAR-2005.

PF 16-AUG-2002; 2002US-00222703.

PR 16-AUG-2002; 2002US-00222703.

XX (MERZ/) MERZOUK A.

PA (HABI/) HABI A.

PA (WONG/) WONG D.

PA (SALA/) SALARI H.

XX Merzouk A, Habi A, Wong D, Salari H;

XX WPI; 2005-232172/24.

XX Chemokine derived analog compound, useful for treating autoimmune
 PT diseases, chronic inflammation, cancer, cardiovascular disease, or
 PT infectious disease.

XX Example 17; Fig 17; 104pp; English.

XX The invention comprises chemokine derived analog peptides, such as
 CC stromal cell-derived factor-1 (SDF-1) peptides or macrophage inflammatory
 CC protein-1-alpha (MIP-1-alpha) peptides. The chemokine derived analog
 CC peptides of the invention are useful for treating inflammation,
 CC autoimmune diseases, cancer, cardiovascular disease, infections,
 CC rheumatoid arthritis, chronic inflammatory bowel disease, chronic
 CC inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis,
 CC atherosclerosis, psoriasis, rhinitis, and organ transplant rejection. The
 CC present amino acid sequence represents a chemokine analog peptide that
 CC was used in an example of the invention.

XX Sequence 26 AA;

Query Match 79.1%; Score 34; DB 9; Length 26;

Best Local Similarity 100.0%; Pred. No. 11;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 VLSYRFP 9

DB 2 VLSYRFP 8

RESULT 14

ADV77013

ID ADY77013 standard; peptide; 26 AA.

XX AC ADY77013;

XX 02-JUN-2005 (first entry)

XX Chemokine analog peptide #102.

XX Chemokine; inflammation; antiinflammatory; autoimmune disease;

KW immunosuppressive; cancer; cytostatic; cardiovascular disease;

KW cardiovascular-gen.; infection; rheumatoid arthritis; antiarthritic;

KW antirheumatic; chronic inflammatory bowel disease; antiinflammatory;

KW gastrointestinal-gen.; multiple sclerosis; neuroprotective; asthma;

KW antiasthmatic; osteoarthritis; osteopathic; atherosclerosis;

KW antiarteriosclerotic; psoriasis; antipsoriatic; rhinitis; antiallergic;

KW organ transplant rejection.

XX Synthetic.

OS Unidentified.

PN US2005059584-A1.

XX 17-MAR-2005.

```

PF 16-AUG-2002; 2002US-00222703.
XX
PR 16-AUG-2002; 2002US-00222703.
XX
PA (MERZ/) MERZOUK A.
PA (HABI/) HABI A.
PA (WONG/) WONG D.
PA (SALA/) SALARI H.
XX
PI Merzouk A, Habi A, Wong D, Salari H;
XX
DR WPI; 2005-232172/24.
XX
PT Chemokine derived analog compound, useful for treating autoimmune
PT diseases, chronic inflammation, cancer, cardiovascular disease, or
PT infectious disease.
XX
PS Example 17; Fig 17; 104pp; English.
XX
CC The invention comprises chemokine derived analog peptides, such as
CC stromal cell-derived factor-1 (SDF-1) peptides or macrophage inflammatory
CC protein-1-alpha (MIP-1-alpha) peptides. The chemokine derived analog
CC peptides of the invention are useful for treating inflammation,
CC autoimmune diseases, cancer, cardiovascular disease, infections,
CC rheumatoid arthritis, chronic inflammatory bowel disease, chronic
CC inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis,
CC atherosclerosis, psoriasis, rhinitis, and organ transplant rejection. The
CC present amino acid sequence represents a chemokine analog peptide that
CC was used in an example of the invention.
XX
SQ Sequence 26 AA;
    Query Match          79.1%; Score 34; DB 9; Length 26;
    Best Local Similarity 100.0%; Pred. No. 11;
    Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 VLSYRF 9
Db 2 VLSYRF 8
    |||||
    |||||

RESULT 15
ID ADY77049
XX ADY77049 standard; peptide; 26 AA.
XX
AC ADY77049;
XX
DT 02-JUN-2005 (first entry)
XX
DE Chemokine analog peptide #138.
XX
KW chemokine; inflammation; antiinflammatory; autoimmune disease;
KW immunosuppressive; cancer; cytostatic; cardiovascular disease;
KW cardiovascular-gen.; infection; rheumatoid arthritis; antiarthritis;
KW antirheumatic; chronic inflammatory bowel disease; antiinflammatory;
KW gastrointestinal-gen.; multiple sclerosis; neuroprotective; asthma;
KW antiasthmatic; osteoarthritis; osteopathic; atherosclerosis;
KW antiarteriosclerotic; psoriasis; antipsoriatic; rhinitis; antiallergic;
KW organ transplant rejection.
XX
OS Synthetic.
OS Unidentified.
XX
PN US2005059584-A1.
XX
PD 17-MAR-2005.
XX
PF 16-AUG-2002; 2002US-00222703.
XX
PR 16-AUG-2002; 2002US-00222703.
XX
PA (MERZ/) MERZOUK A.
PA (HABI/) HABI A.

```

```

PA (WONG/) WONG D.
PA (SALA/) SALARI H.
XX
PI Merzouk A, Habi A, Wong D, Salari H;
XX
DR WPI; 2005-232172/24.
XX
PT Chemokine derived analog compound, useful for treating autoimmune
PT diseases, chronic inflammation, cancer, cardiovascular disease, or
PT infectious disease.
XX
PS Example 17; Fig 17; 104pp; English.
XX
CC The invention comprises chemokine derived analog peptides, such as
CC stromal cell-derived factor-1 (SDF-1) peptides or macrophage inflammatory
CC protein-1-alpha (MIP-1-alpha) peptides. The chemokine derived analog
CC peptides of the invention are useful for treating inflammation,
CC autoimmune diseases, cancer, cardiovascular disease, infections,
CC rheumatoid arthritis, chronic inflammatory bowel disease, chronic
CC inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis,
CC atherosclerosis, psoriasis, rhinitis, and organ transplant rejection. The
CC present amino acid sequence represents a chemokine analog peptide that
CC was used in an example of the invention.
XX
SQ Sequence 26 AA;
    Query Match          79.1%; Score 34; DB 9; Length 26;
    Best Local Similarity 100.0%; Pred. No. 11;
    Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 VLSYRF 9
Db 2 VLSYRF 8
    |||||
    |||||

Search completed: August 10, 2006, 23:00:39
Job time : 120.273 secs

```

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 10, 2006, 23:13:31 ; Search time 16.3636 Seconds
(without alignments)
37.022 Million cell updates/sec

Title: US-10-825-603-1

Perfect score: 43

Sequence: 1 RSVLSYRF 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 239914 seqs, 67312017 residues

Total number of hits satisfying chosen parameters: 239914

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New.*

1: /EMC_Celerra_SID33/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
2: /EMC_Celerra_SID33/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
3: /EMC_Celerra_SID33/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
4: /EMC_Celerra_SID33/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
5: /EMC_Celerra_SID33/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
6: /EMC_Celerra_SID33/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
7: /EMC_Celerra_SID33/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
8: /EMC_Celerra_SID33/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	72.1	372	7	US-11-056-355B-81312
2	31	72.1	439	7	US-11-056-355B-81311
3	31	72.1	441	7	US-11-056-355B-81310
4	31	72.1	483	7	US-11-330-403-16842
5	31	72.1	484	7	US-11-330-403-4463
6	31	72.1	484	7	US-11-330-403-5632
7	31	72.1	484	7	US-11-330-403-7972
8	31	72.1	484	7	US-11-330-403-8319
9	31	72.1	484	7	US-11-330-403-18291
10	30	69.8	262	6	US-10-953-349-10285
11	30	69.8	262	7	US-11-056-355B-49774
12	30	69.8	262	7	US-11-056-355B-88515
13	30	69.8	262	7	US-11-056-355B-92271
14	30	69.8	262	6	US-10-953-349-10284
15	30	69.8	282	7	US-11-056-355B-49773
16	30	69.8	282	7	US-11-056-355B-88514
17	30	69.8	282	7	US-11-056-355B-92270
18	30	69.8	283	6	US-10-953-349-10283
19	30	69.8	283	7	US-11-056-355B-49772
20	30	69.8	283	7	US-11-056-355B-88513
21	30	69.8	283	7	US-11-056-355B-92269
22	30	69.8	568	7	US-11-233-089-2
23	30	69.8	568	7	US-11-233-089-4
24	30	69.8	942	6	US-10-449-902-52959
25	30	69.8	991	6	US-10-449-902-41190

26 29 67.4 73 6 US-10-196-749-396 Sequence 396, App
27 29 67.4 73 7 US-11-101-316-148 Sequence 148, App
28 29 67.4 73 7 US-11-376-673-148 Sequence 148, App
29 29 67.4 79 7 US-11-056-355B-21714 Sequence 21714, A
30 29 67.4 93 6 US-10-505-928-112 Sequence 112, App
31 29 67.4 93 6 US-10-511-937-2454 Sequence 2454, Ap
32 29 67.4 138 7 US-11-056-355B-107948 Sequence 107948,
33 29 67.4 138 7 US-11-056-355B-119187 Sequence 119187,
34 29 67.4 147 7 US-11-056-355B-107947 Sequence 107947,
35 29 67.4 147 7 US-11-056-355B-119186 Sequence 119186,
36 29 67.4 429 7 US-11-330-403-8035 Sequence 8035, Ap
37 29 67.4 458 7 US-11-317-571-147 Sequence 147, App
38 29 67.4 483 6 US-10-449-902-44566 Sequence 44566, A
39 29 67.4 499 7 US-11-317-789A-221 Sequence 221, App
40 29 67.4 526 7 US-11-056-355B-87100 Sequence 87100, A
41 29 67.4 527 7 US-11-056-355B-87012 Sequence 87012, A
42 29 67.4 546 7 US-11-056-355B-87099 Sequence 87099, A
43 29 67.4 547 7 US-11-056-355B-87011 Sequence 87011, A
44 29 67.4 595 7 US-11-056-355B-87098 Sequence 87098, A
45 29 67.4 596 7 US-11-056-355B-69860 Sequence 69860, A

ALIGNMENTS

RESULT 1
US-11-056-355B-81312
; Sequence 81312, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 81312
; LENGTH: 372
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(372)
; OTHER INFORMATION: Ceres Seq. ID no. 12659264
US-11-056-355B-81312

Query Match 72.1%; Score 31; DB 7; Length 372;
Best Local Similarity 75.0%; Pred. NO. 75;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 RSVLSYR 8
DB 318 RSVLSYQ 325

RESULT 2
US-11-056-355B-81311
; Sequence 81311, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13

```

; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 81311
; LENGTH: 439
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(439)
; OTHER INFORMATION: Ceres Seq. ID no. 12659263
US-11-056-355B-81311

Query Match          72.1%; Score 31; DB 7; Length 439;
Best Local Similarity 75.0%; Pred. No. 90;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSVSLSYR 8
    |||||:
Db 385 RSVSISYQ 392

RESULT 3
US-11-056-355B-81310
; Sequence 81310, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 81310
; LENGTH: 441
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(441)
; OTHER INFORMATION: Ceres Seq. ID no. 12659262
US-11-056-355B-81310

Query Match          72.1%; Score 31; DB 7; Length 441;
Best Local Similarity 75.0%; Pred. No. 90;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSVSLSYR 8
    |||||:
Db 387 RSVSISYQ 394

RESULT 4
US-11-330-403-16842
; Sequence 16842, Application US/11330403
; Publication No. US20060159563A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53629)B
; CURRENT APPLICATION NUMBER: US/11/330,403
; CURRENT FILING DATE: 2006-01-12
; NUMBER OF SEQ ID NOS: 19250
; SEQ ID NO 16842
; LENGTH: 483
; TYPE: prt
; ORGANISM: Proteus mirabilis
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(483)
; OTHER INFORMATION: unsure at all Xaa locations
US-11-330-403-16842

Query Match          72.1%; Score 31; DB 7; Length 483;
Best Local Similarity 66.7%; Pred. No. 99;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RSVSLSYRF 9
    | : |||||
Db 181 RGLPLSYRF 189

RESULT 5
US-11-330-403-4463
; Sequence 4463, Application US/11330403
; Publication No. US20060159563A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53629)B
; CURRENT APPLICATION NUMBER: US/11/330,403
; CURRENT FILING DATE: 2006-01-12
; NUMBER OF SEQ ID NOS: 19250
; SEQ ID NO 4463
; LENGTH: 484
; TYPE: prt
; ORGANISM: Proteus mirabilis
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(484)
; OTHER INFORMATION: unsure at all Xaa locations
US-11-330-403-4463

Query Match          72.1%; Score 31; DB 7; Length 484;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RSVSLSYRF 9
    | : |||||
Db 182 RGLPLSYRF 190

RESULT 6
US-11-330-403-5632
; Sequence 5632, Application US/11330403
; Publication No. US20060159563A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53629)B
; CURRENT APPLICATION NUMBER: US/11/330,403
; CURRENT FILING DATE: 2006-01-12
; NUMBER OF SEQ ID NOS: 19250
; SEQ ID NO 5632
; LENGTH: 484
; TYPE: prt
; ORGANISM: Proteus mirabilis
US-11-330-403-5632

Query Match          72.1%; Score 31; DB 7; Length 484;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RSVSLSYRF 9
    | : |||||
Db 182 RGLPLSYRF 190

RESULT 7
US-11-330-403-7972
; Sequence 7972, Application US/11330403
; Publication No. US20060159563A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.

```

; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53629)B
; CURRENT APPLICATION NUMBER: US/11/330,403
; CURRENT FILING DATE: 2006-01-12
; NUMBER OF SEQ ID NOS: 19250
; SEQ ID NO 7972
; LENGTH: 484
; TYPE: PRT
; ORGANISM: Proteus mirabilis
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(484)
; OTHER INFORMATION: unsure at all Xaa locations
US-11-330-403-7972

Query Match 72.1%; Score 31; DB 7; Length 484;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RSVLSLYRF 9
| : |||||
Db 182 RGLPLSYRF 190

RESULT 8

US-11-330-403-8319
; Sequence 8319, Application US/11330403
; Publication No. US20060159563A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53629)B
; CURRENT APPLICATION NUMBER: US/11/330,403
; CURRENT FILING DATE: 2006-01-12
; NUMBER OF SEQ ID NOS: 19250
; SEQ ID NO 8319
; LENGTH: 484
; TYPE: PRT
; ORGANISM: Proteus mirabilis
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(484)
; OTHER INFORMATION: unsure at all Xaa locations
US-11-330-403-8319

Query Match 72.1%; Score 31; DB 7; Length 484;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RSVLSLYRF 9
| : |||||
Db 182 RGLPLSYRF 190

RESULT 9

US-11-330-403-18291
; Sequence 18291, Application US/11330403
; Publication No. US20060159563A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53629)B
; CURRENT APPLICATION NUMBER: US/11/330,403
; CURRENT FILING DATE: 2006-01-12
; NUMBER OF SEQ ID NOS: 19250
; SEQ ID NO 18291
; LENGTH: 484
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-11-330-403-18291

Query Match 72.1%; Score 31; DB 7; Length 484;
Best Local Similarity 66.7%; Pred. No. 1e+02;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 RSVLSLYRF 9
| : |||||
Db 182 RGLPLSYRF 190

RESULT 10

US-10-953-349-10285
; Sequence 10285, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10285
; LENGTH: 262
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-10285

Query Match 69.8%; Score 30; DB 6; Length 262;
Best Local Similarity 66.7%; Pred. No. 84;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RSVLSLYRF 9
| : |||||
Db 174 RSSSLAFRF 182

RESULT 11

US-11-056-355B-49774
; Sequence 49774, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 49774
; LENGTH: 262
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(262)
; OTHER INFORMATION: Ceres Seq. ID no. 13648120
US-11-056-355B-49774

Query Match 69.8%; Score 30; DB 7; Length 262;
Best Local Similarity 66.7%; Pred. No. 84;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RSVLSLYRF 9
| : |||||
Db 174 RSSSLAFRF 182

RESULT 12

US-11-056-355B-88515
; Sequence 88515, Application US/11056355B
; Publication No. US20060150283A1

```
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; PRIOR FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 88515
; LENGTH: 262
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(262)
; OTHER INFORMATION: Ceres Seq. ID no. 12710126
US-11-056-355B-88515

Query Match      69.8%; Score 30; DB 7; Length 262;
Best Local Similarity 66.7%; Pred. No. 84;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 RVSLSYRF 9
Db      174 RSSSLAFRF 182

RESULT 13
US-11-056-355B-92271
; Sequence 92271, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; PRIOR FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 92271
; LENGTH: 262
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(262)
; OTHER INFORMATION: Ceres Seq. ID no. 12710126
US-11-056-355B-92271

Query Match      69.8%; Score 30; DB 7; Length 262;
Best Local Similarity 66.7%; Pred. No. 84;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 RVSLSYRF 9
Db      174 RSSSLAFRF 182

RESULT 14
US-10-953-349-10284
; Sequence 10284, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
```

```
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10284
; LENGTH: 282
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
US-10-953-349-10284

Query Match      69.8%; Score 30; DB 6; Length 282;
Best Local Similarity 66.7%; Pred. No. 91;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 RVSLSYRF 9
Db      194 RSSSLAFRF 202

RESULT 15
US-11-056-355B-49773
; Sequence 49773, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 49773
; LENGTH: 282
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(282)
; OTHER INFORMATION: Ceres Seq. ID no. 13648119
US-11-056-355B-49773

Query Match      69.8%; Score 30; DB 7; Length 282;
Best Local Similarity 66.7%; Pred. No. 91;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 RVSLSYRF 9
Db      194 RSSSLAFRF 202

Search completed: August 10, 2006, 23:20:43
Job time : 16.3636 secs
```

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 10, 2006, 22:53:25 ; Search time 100 Seconds
(without alignments)
55.501 Million cell updates/sec

Title: US-10-825-603-3

Perfect score: 28

Sequence: 1 VLSYSR 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 7.2.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	100.0	89	1	SDF1_MOUSE
2	28	100.0	89	2	Q6ICW0_HUMAN
3	28	100.0	89	2	Q3LSL5_CANPA
4	28	100.0	89	2	Q5XNN9_CANPA
5	28	100.0	89	2	Q8HYPO_MACMU
6	28	100.0	89	2	Q543V6_MOUSE
7	28	100.0	89	2	Q902D1_RAT
8	28	100.0	90	2	Q2L986_HUMAN
9	28	100.0	92	2	Q9H554_HUMAN
10	28	100.0	93	1	SDF1_FELCA
11	28	100.0	93	1	SDF1_HUMAN
12	28	100.0	93	2	Q3LSL4_CANPA
13	28	100.0	93	2	Q588M6_PONPY
14	28	100.0	93	2	Q4FJL5_MOUSE
15	28	100.0	100	2	Q2L985_HUMAN
16	28	100.0	116	2	Q6EKW4_PIG
17	28	100.0	119	2	Q5IT36_HUMAN
18	28	100.0	119	2	Q80YV8_RAT
19	28	100.0	140	2	Q2L988_HUMAN
20	28	100.0	157	2	Q8D9U8_VIBVU
21	28	100.0	172	2	Q5GD95_XENNE
22	28	100.0	172	2	Q72350_VIBCH
23	28	100.0	172	2	Q7N9G3_PHOLL
24	28	100.0	189	2	Q4CAP4_CROWT
25	28	100.0	190	2	Q4CH68_CLOTH
26	28	100.0	218	2	Q9JU28_NEIMA
27	28	100.0	218	2	Q9JZX8_NEIMA
28	28	100.0	274	2	Q8D929_VIBVU
29	28	100.0	298	2	Q7VJQ5_HELHP
30	28	100.0	299	2	Q9RBF7_RALEU
31	28	100.0	333	2	Q61X64_CABER

32	28	100.0	347	2	Q01853_CABEL
33	28	100.0	364	1	REC4_PORGI
34	28	100.0	373	2	Q3RXG7_RALME
35	28	100.0	435	2	Q821S4_SALTI
36	28	100.0	439	2	Q85313_SALTY
37	28	100.0	439	2	Q57GM8_SALCH
38	28	100.0	439	2	Q5PIX7_SALPA
39	28	100.0	439	2	Q8ZKG7_SALTY
40	28	100.0	468	2	Q23425_ARATH
41	28	100.0	586	1	ACES_TORCA
42	28	100.0	589	2	Q83ZV8_MYCSM
43	28	100.0	590	1	ACES_TORMA
44	28	100.0	606	1	ACES_BUNFA
45	28	100.0	607	2	Q65XH2_ORYSA

ALIGNMENTS

RESULT 1
SDF1_MOUSE
ID SDF1_MOUSE STANDARD; PRT; 89 AA.
AC P40224;
DT 01-FEB-1995, integrated into UniProtKB/Swiss-Prot.
DT 01-FEB-1995, sequence version 1.
DT 07-FEB-2006, entry version 51.
DE Stromal cell-derived factor 1 precursor (SDF-1) (CXCL12) (Pre-B cell
DE growth-stimulating factor) (PBSF) (12-O-tetradecanoylphorbol 13-
DE acetate repressed protein 1) (TPAR1) (Thymic lymphoma cell-stimulating
DE factor) (TISF).
GN Name=Cxcl12; Synonyms=Sdf1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RX MEDLINE=94181581; PubMed=8134392;
RA Nagasawa T., Kikutani H., Kishimoto T.;
RT "Molecular cloning and structure of a pre-B-cell growth-stimulating
RT factor".
RL Proc. Natl. Acad. Sci. U.S.A. 91:2305-2309(1994).
[2]
RP NUCLEOTIDE SEQUENCE [MRNA].
RX MEDLINE=93342488; PubMed=8342023;
RA Tashiro K., Tada H., Heilker R., Shirozu M., Nakano T., Honjo T.;
RT "Signal sequence trap: a cloning strategy for secreted proteins and
RT type I membrane proteins.";
RL Science 261:600-603(1993).
[3]
RP NUCLEOTIDE SEQUENCE [MRNA].
RX MEDLINE=95073497; PubMed=7982471; DOI=10.1006/excr.1994.1344;
RA Jiang W., Zhou P., Kahn S.M., Tomita N., Johnson M.D., Weinstein I.B.;
RT "Molecular cloning of TPAP1, a gene whose expression is repressed by
RT the tumor promoter 12-O-tetradecanoylphorbol 13-acetate (TPA).";
RL Exp. Cell Res. 215:284-293(1994).
[4]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC STRAIN=AKR/J;
RA Nomura M., Nakata Y., Urawa A., Nose M., Akashi M., Suzuki G.;
RN Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
[5]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM ALPHA).
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RX PubMed=16141072; DOI=10.1126/science.1113014;
RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA Davis M.J., Wilming L.G., Batalov S., Allen J.E.,
RA Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,

RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA Guscinich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA Hill D., Huminecki L., Iacono M., Ieko K., Iwama A., Ishikawa T.,
RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kello J., Kitamura H.,
RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA Motcagui-Tabar S., Mulder N., Nakano N., Nakachi H., Ng P.,
RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavese G., Pesole G.,
RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA Rost B., Ruan Y., Salzberg S.L., Sanderlin A., Schneider C.,
RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA Sperling S., Stupka E., Sugita K., Sultana R., Takenaka Y., Taki K.,
RA Tannoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA Wahlesed C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA Fukuda S., Kanamori-Katsuyama M., Suzuki M., Aoki J., Arakawa T.,
RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashita N.,
RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Nimomiya N.,
RA Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,
RA Tagami M., Waki K., Wataniki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA Hayashizaki Y.;
RT "The transcriptional landscape of the mammalian genome.";
RL Science 309:1559-1563 (2005).
RN [6]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM ALPHA).
RC STRAIN=C57BL/6J; TISSUE=Mammary gland;
RX MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,
RA Schnerch A., Schein J.E., Jones S.J.W., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -!- FUNCTION: Chemoattractant active on T-lymphocytes, monocytes, but
CC not neutrophils.
CC -!- FUNCTION: Stimulates the proliferation of bone marrow-derived b
CC progenitor cells in the presence of IL-7 as well as growth of the
CC stromal cell-dependent B-cell clone DW34 cells.
CC -!- SUBCELLULAR LOCATION: Secreted protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=alternative splicing; Named isoforms=2;
CC Name=alpha;
CC IsoId=P40224-1; Sequence=Displayed;
CC Name=Beta;
CC IsoId=P40224-2; Sequence=VSP_001057;
CC -!- SIMILARITY: Belongs to the interleukin alpha (chemokine Cxk)
CC family.
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License

CC -----
DR EMBL: D21072; BAA04648.1; -; mRNA.
DR EMBL: L12029; AAA40100.1; -; mRNA.
DR EMBL: L12030; AAA40101.1; -; mRNA.
DR EMBL: S74318; AAB32650.1; -; mRNA.
DR EMBL: D43804; BAA07862.1; -; mRNA.
DR EMBL: D43805; BAA07863.1; -; mRNA.
DR EMBL: AK075596; BAC35845.1; -; mRNA.
DR EMBL: BC006640; AAH06640.1; -; mRNA.
DR PIR: A53497; A53497.
DR PIR: I81182; I81182.
DR HSSP: P40061; 1SDF.
DR SMR: P40224; 23-88.
DR Ensembl: ENSMUSG00000061353; Mus musculus.
DR MGI: MGI-103556; Cxcl12.
DR GO: GO:0005635; C:extracellular space; TAS.
DR GO: GO:0008009; P:chemokine activity; IDA.
DR GO: GO:0001667; P:ameboid cell migration; IMP.
DR GO: GO:0007420; P:brain development; IDA.
DR GO: GO:0007281; P:germ cell development; IDA.
DR GO: GO:0008354; P:germ cell migration; IDA.
DR GO: GO:0050930; P:induction of positive chemotaxis; IDA.
DR GO: GO:0001569; P:patterning of blood vessels; IMP.
DR GO: GO:0003035; P:positive regulation of cell migration; IDA.
DR GO: GO:0042038; P:T cell proliferation; IMP.
DR InterPro: IPR002473; C-X-C/Interlkn_8.
DR InterPro: IPR001811; Chemokine IL8.
DR InterPro: IPR001089; CXC_chemokine_sm1.
DR Pfam: PF00048; IL8; 1.
DR PRINTS: PR00436; INTERLEUKIN8.
DR SMART: SM00199; SCY; 1.
DR PROSITE: PS00471; SMALL CYTOKINES CXC; FALSE NEG.
KW Alternative splicing; Chemotaxis; Cytokine; Growth factor;
KW Sensory transduction; Signal.
FT SIGNAL 1 21 Potential.
FT CHAIN 22 89 Stromal cell-derived factor 1.
FT FTID=PRO_0000005112.
FT DISULFID 30 55 By similarity.
FT DISULFID 32 71 By similarity.
FT VARSPPLIC 89 89 K->KRLKM (in isoform Beta).
FT FTID=VSP_001057.
SQ SEQUENCE 89 AA; 10032 MW; C4B8AD69078E55FA CRC64;
Query Match 100.0%; Score 28; DB 1; Length 89;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VLSYR 6
Db 24 VLSYR 29
RESULT 2
O6ICW0 HUMAN
ID O6ICW0 HUMAN PRELIMINARY; PRT; 89 AA.
AC O6ICW0;
DT 10-MAY-2005, integrated into UniProtKB/TREMBL.
DT 10-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 5.
DE CXCL12 protein (stromal cell-derived factor 1a) (Fragment).
GN Name=CXCL12;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Ebert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Zhao X., Zhang H., Lee S., Wong K., Zheng B.;


```
RT "Polymorphism study of cell-derived factor 1 (SDF1) gene and their
RL correlation with HIV infection in a Chinese cohort";
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; CR450283; CAG29279.1; -; mRNA.
DR EMBL; AY874118; AAW82036.1; -; mRNA.
DR SNR; Q6ICW0; 23-88.
DR Ensembl; ENSG00000107562; Homo sapiens.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0008009; F:chemokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR002473; C-X-C/Interlkn_8.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR PRINTS; PR00436; INTERLEUKINS.
DR SMART; SM00199; SCY; 1.
FT NON TER 89
SQ SEQUENCE 89 AA; 10103 MW; 62B44E8D209C3A14 CRC64;

Query Match 100.0%; Score 28; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLSYR 6
DB 24 VLSYR 29

RESULT 3
Q3LSL5 CANFA PRELIMINARY; PRT; 89 AA.
AC Q3LSL5;
DT 25-OCT-2005, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 3.
DE Chemokine (C-X-C motif) ligand 12 isoform alpha.
GN Name=CXCL12;
OC Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
NUCLEOTIDE SEQUENCE.
RA Tsuchida S., Kagi A., Takahashi T.;
RT "Evaluation of the canine CXCR4 and CXCL12 genes as a candidate for
RT chronic neutropenia with myelokathexis in a border collie dog.";
RL Submitted (AUG-2005) to the EMBL/GenBank/DBJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; DQ182700; ABA29310.1; -; mRNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0008009; F:chemokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR002473; C-X-C/Interlkn_8.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR PRINTS; PR00436; INTERLEUKINS.
DR SMART; SM00199; SCY; 1.
SQ SEQUENCE 89 AA; 10028 MW; B1F8D2D64D36B496 CRC64;

Query Match 100.0%; Score 28; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLSYR 6
DB 24 VLSYR 29

"Polymorphism study of cell-derived factor 1 (SDF1) gene and their
RL correlation with HIV infection in a Chinese cohort";
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; CR450283; CAG29279.1; -; mRNA.
DR EMBL; AY874118; AAW82036.1; -; mRNA.
DR SNR; Q6ICW0; 23-88.
DR Ensembl; ENSG00000107562; Homo sapiens.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0008009; F:chemokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR002473; C-X-C/Interlkn_8.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR PRINTS; PR00436; INTERLEUKINS.
DR SMART; SM00199; SCY; 1.
FT NON TER 89
SQ SEQUENCE 89 AA; 10103 MW; 62B44E8D209C3A14 CRC64;

Query Match 100.0%; Score 28; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLSYR 6
DB 24 VLSYR 29

RESULT 4
Q5XNN9 CANFA PRELIMINARY; PRT; 89 AA.
AC Q5XNN9;
DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.
DT 01-FEB-2005, sequence version 2.
DT 07-FEB-2006, entry version 8.
DE Stromal cell-derived factor-1.
DE Canis familiaris (Dog).
DE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
DE Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
DE Canis.
OX NCBI_TaxID=9615;
RN [1]
NUCLEOTIDE SEQUENCE.
RA Wei Y., Hu S.;
RT "Identification and cloning of dog SDF-1 cDNA.";
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AY746395; AAU89475.2; -; mRNA.
DR SNR; Q5XNN9; 23-88.
DR Ensembl; ENSCAPG0000007026; Canis familiaris.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0008009; F:chemokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR002473; C-X-C/Interlkn_8.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR PRINTS; PR00436; INTERLEUKINS.
DR SMART; SM00199; SCY; 1.
SQ SEQUENCE 89 AA; 10005 MW; E9B8AD69078E4020 CRC64;

Query Match 100.0%; Score 28; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLSYR 6
DB 24 VLSYR 29

RESULT 5
Q8HYPO MACMU PRELIMINARY; PRT; 89 AA.
AC Q8HYPO;
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2003, sequence version 1.
DT 07-FEB-2006, entry version 13.
DE Chemokine CXCL12/SDF-1ALPHA.
DE Macaca mulatta (Rhesus macaque).
DE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
DE Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
DE Cercopithecoidea; Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
NUCLEOTIDE SEQUENCE.
RA Basu S., Schaefer T.M., Ghosh M., Fuller C.L., Reinhart T.A.;
RT "Molecular cloning and sequencing of 25 different rhesus macaque
RT chemokine cDNAs reveals evolutionary conservation among C, CC, CXCL
RT and CX3C families of chemokines.";
RL Cytokine 18:140-148(2002).
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AF449283; AAN76086.1; -; mRNA.
DR HSP; P48061; ISDF.
```

DR SMR; Q8HYPO; 23-88.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0008009; F:chemokine activity; IEA.
DR GO; GO:0006995; F:immune response; IEA.
DR InterPro; IPR002473; C-X-C/Interlkn_8.
DR InterPro; IPR001811; C:chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR PRINTS; PR00436; INTERLEUKIN8.
DR SMART; SM00199; SCY; 1.
SQ SEQUENCE 89 AA; 10105 MW; AD531633C6DC2B07 CRC64;

Query Match 100.0%; Score 28; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLSYR 6
| | | | |
Db 24 VLSYR 29

RESULT 6
Q543V6 MOUSE
ID Q543V6 MOUSE PRELIMINARY; PRT; 89 AA.
AC Q543V6;
DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 24-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE 9.5 days embryo parthenogenote cDNA, RIKEN full-length enriched
DE library, clone.B130032A21 product:stromal cell derived factor 1, full
DE insert sequence.
GN Name=Cxcl12;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;
RX PubMed=98279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Methods Enzymol. 303:19-44(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;
RX PubMed=16141072; DOI=10.1126/science.1112014;
RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E., Ambesi-Impombato A., Apweiler R., Auraliya R.N., Bailey T.L.,
RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA di Bernardo D., Down T., Engstrom P., Fagioli M., Paulkner G.,
RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA Guerginich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA Hill D., Humnietek L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kello J., Kitamura H.,
RA Kitano H., Kollas G., Kriehn S.P., Kruger A., Kummerfeld S.K.,
RA Kurochkin I.V., Larau L.F., Lazarevic D., Lipovich L., Liu J.,
RA Liuni S., McWilliam M., Madan Babu M., Madera M., Marchionni L.,
RA Matsuda H., Matsuzawa S., Miki H., Mignone N., Miyake S., Morris K.,
RA Mottagui-Tabar S., Mulder N., Nakano N., Nakaura H., Ng P.,
RA Nilleson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavese G., Pesole G.,
RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA Sperling S., Stupka E., Sugliura K., Sultana R., Takenaka Y., Taki K.,

RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA Yananishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Nimomiya N.,
RA Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA Tagami M., Waki K., Watanabe A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA Hayashizaki Y.;
RT "The transcriptional landscape of the mammalian genome.";
RL Science 309:1559-1563(2005).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;
RX PubMed=16141073; DOI=10.1126/science.1112009;
RG RIKEN Genome Exploration Research Group, and Genome Science Group
RG (Genome Network Core Team) and the FANTOM Consortium;
RT "Antisense Transcription in the Mammalian Transcriptome.";
RL Science 309:1564-1566(2005).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaide I., Osato N., Saito R., Suzuki H., Yananaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ring B.Z., Ringwald M.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang L., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aizawa K., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yananaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bona M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohseki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 [6]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 [7]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 [8]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Inotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito K., Saitoh C., Sakai K., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 CC
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC
 CC EMBL; AK045092; BAC32216.1; -; mRNA.
 DR SMR; Q543V6; 23-88.
 DR Ensembl; ENSMUSG00000061353; Mus musculus.
 DR MGI; MGI:103556; Cxcl12.
 DR GO; GO:0005615; C:extracellular space; RCA.
 DR GO; GO:0008009; F:chemokine activity; IDA.
 DR GO; GO:0001667; P:ameboid cell migration; IMP.
 DR GO; GO:0007420; P:brain development; IDA.
 DR GO; GO:0007281; P:germ cell development; IDA.
 DR GO; GO:0008354; P:germ cell migration; IDA.
 DR GO; GO:0009330; P:induction of positive chemotaxis; IDA.
 DR GO; GO:0001569; P:patterning of blood vessels; IMP.
 DR GO; GO:0003035; P:positive regulation of cell migration; IDA.
 DR GO; GO:0042098; P:T cell proliferation; IMP.
 DR InterPro; IPR002473; C-X-C/interlkn_8.
 DR InterPro; IPR001811; Chemokine_IL8.
 DR Pfam; PF00048; IL8; 1.
 DR PRINTS; PR000436; INTERLEUKIN8.
 DR SMART; SM00199; SCV; 1.
 DR SEQUENCE 89 AA; 10032 MW; C4B8AD69078E5FA CRC64;
 SQ
 Query Match 100.0%; Score 28; DB 2; Length 89;
 Best Local Similarity 100.0%; Pred. No. 72;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VLSLYR 6

Db 24 VLSLYR 29
 RESULT 7
 Q9QZD1_RAT PRELIMINARY; PRT; 89 AA.
 AC Q9QZD1_RAT
 DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
 DT 01-MAY-2000, sequence version 1.
 DT 07-FEB-2006, entry version 22.
 DE Stromal cell-derived factor-1 alpha (Chemokine (C-X-C motif) ligand
 DE 12).
 GN Name=Cxcl12; Synonyms=SDF-1;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidae; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=101116;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Sprague-Dawley;
 RA Ohtani Y., Okada M., Kawaguchi N., Minami M., Satoh M.;
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Pillariseti K., Gupta S.K.;
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 [3]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Kidney;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueidi T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [4]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Kidney;
 RA Director MGC Project;
 RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
 CC
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC
 CC EMBL; AF189724; AAF01066.1; -; mRNA.
 DR EMBL; AF209976; AAG43506.1; -; mRNA.
 DR EMBL; BC078737; AAH78737.1; -; mRNA.
 DR HSSP; P48061; 1SDF.
 DR SMR; Q9QZD1; 23-88.
 DR Ensembl; ENSRNOG00000013589; Rattus norvegicus.
 DR RGD; 3651; Cxcl12.
 DR GO; GO:0008009; F:chemokine activity; TAS.
 DR GO; GO:0007420; P:brain development; IEP.
 DR GO; GO:0001764; P:neuron migration; IDA.
 DR InterPro; IPR002473; C-X-C/interlkn_8.
 DR InterPro; IPR001811; Chemokine_IL8.

```
DR Pfam; PF00048; IL8; 1.
DR PRINTS; PR00436; INTERLEUKIN8.
DR SMART; SM00199; SCY; 1.
SQ SEQUENCE 89 AA; 9777 MW; D86777626A2E35FA CRC64;

Query Match 100.0%; Score 28; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSLSYR 6
DB 24 VSLSYR 29

RESULT 8
Q2L986 HUMAN PRELIMINARY; PRT; 90 AA.
AC Q2L986;
DT 21-FEB-2006, integrated into UniProtKB/TrEMBL.
DT 21-FEB-2006, sequence version 1.
DT 21-FEB-2006, entry version 1.
DE Stromal cell-derived factor 1 epsilon.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Yu L., Cecil J., Peng S.-B., Schrementia J., Kovacevic S., Paul D.,
RA Su E.W., Wang J.;
RT "Identification and expression of novel isoforms of human stromal
RT cell-derived factor 1."
RL Submitted (DEC-2005) to the EMBL/GenBank/DBJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NonDerivs License
CC -----
DR EMBL; DQ345519; ABC69272.1; -; mRNA.
SQ SEQUENCE 90 AA; 10192 MW; 7375C44E8D209C3A CRC64;

Query Match 100.0%; Score 28; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSLSYR 6
DB 24 VSLSYR 29

RESULT 9
Q9H554 HUMAN PRELIMINARY; PRT; 92 AA.
AC Q9H554;
DT 01-MAR-2001, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2001, sequence version 1.
DT 07-FEB-2006, entry version 21.
DE Chemokine (C-X-C motif) ligand 12 (Stromal cell-derived factor 1).
GN Name=CXCL12; ORFNames=RP11-20J15.4-002;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Bird C.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NonDerivs License
CC -----
DR EMBL; AL137026; CAC10202.1; -; Genomic_DNA.

DR HSSP; P48061; LSDF.
DR SMR; Q9H554; 23-88.
DR Ensembl; ENSG00000107562; Homo sapiens.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0008009; P:chemokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR002473; C-X-C/Interlkn_8.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR PRINTS; PR00436; INTERLEUKIN8.
DR SMART; SM00199; SCY; 1.
SQ SEQUENCE 92 AA; 10510 MW; AEF0C402B44E8D20 CRC64;

Query Match 100.0%; Score 28; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSLSYR 6
DB 24 VSLSYR 29

RESULT 10
SDF1_FELCA
ID SDF1_FELCA STANDARD; PRT; 93 AA.
AC O62657; O54AJ3;
DT 15-DEC-1998, integrated into UniProtKB/Swiss-Prot.
DT 01-AUG-1998, sequence version 1.
DT 07-MAR-2006, entry version 39.
DE Stromal cell-derived factor 1 precursor (SDF-1) (CXCL12).
GN Name=CXCL12; Synonyms=SDF1;
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
OC Felinae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS ALPHA AND BETA).
RC TISSUE=Thymus;
RX MEDLINE=98450506; PubMed=9777331;
RA DOI=10.1046/j.1365-2370.1998.00107.x;
RA Nishimura Y., Miyazawa T., Ikeda Y., Izumiya Y., Nakamura K.,
RA Cai J.-S., Sato E., Kohmoto M., Mikami T.;
RT "Molecular cloning and sequencing of feline stromal cell-derived
RT factor-1 alpha and beta."
RL Eur. J. Immunogenet. 25:303-305 (1998).
CC -----
CC FUNCTION: Chemoattractant active on T-lymphocytes, monocytes, but
CC not neutrophils.
CC -!- SUBCELLULAR LOCATION: Secreted protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Beta; Synonyms=SDF-lb;
CC IsoId=O62657-1; Sequence=Displayed;
CC Name=Alpha; Synonyms=SDF-la;
CC IsoId=O62657-2; Sequence=VSP_001055;
CC -!- SIMILARITY: Belongs to the interleukin alpha (chemokine Cx)
CC family.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NonDerivs License
CC -----
DR EMBL; AB011965; BAA28601.1; -; mRNA.
DR EMBL; AB011966; BAA28602.1; -; mRNA.
DR HSSP; P48061; LSDF.
DR SMR; O62657; 23-88.
DR InterPro; IPR002473; C-X-C/Interlkn_8.
DR InterPro; IPR001811; Chemokine_IL8.
DR InterPro; IPR001089; CXCL12.
DR Pfam; PF00048; IL8; 1.
DR PRINTS; PR00436; INTERLEUKIN8.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00471; SMALL_CYTOKINES_CXC; FALSE NEG.
KW Alternative splicing; Chemotaxis; Cytokine; Growth factor;
```

KW Sensory transduction; Signal.
 FT SIGNAL 1 21 Potential.
 FT CHAIN 22 93 Stromal cell-derived factor 1.
 FT FTID=PRO_0000005108.
 FT DISULFID 30 55 By similarity.
 FT DISULFID 32 71 By similarity.
 FT VARSPLIC 90 93 Missing (in isoform Alpha).
 FT FTID=VSP_001055
 SQ SEQUENCE 93 AA; 10581 MW; 44FC76371E9BE37 CRC64;
 Query Match 100.0%; Score 28; DB 1; Length 93;
 Best Local Similarity 100.0%; Pred. No. 75;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VLSLSR 6
 Db 24 VLSLSR 29
 RESULT 11
 SDF1_HUMAN STANDARD; PRT; 93 AA.
 AC P48061;
 DT 01-FEB-1996, integrated into UniProtKB/Swiss-Prot.
 DT 01-FEB-1996, sequence version 1.
 DT 21-FEB-2006, entry version 58.
 DE Stromal cell-derived factor 1 precursor (SDF-1) (CXCL12) (Pre-B cell
 DE growth-stimulating factor) (PBSP) (HHRH) [Contains: SDF-1-beta(3-72);
 DE SDF-1-alpha(3-67)].
 GN Name=CXCL12; Synonyms=SDF1;
 OS Homo sapiens (Human).
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Sporila L.D.;
 RL Submitted (OCT-1994) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=96039262; PubMed=7490086;
 RA Shirozu M., Nakano T., Inazawa J., Tashiro K., Tada H., Shinohara T.,
 RA Honjo T.;
 RT Structure and chromosomal localization of the human stromal cell-
 RT derived factor 1 (SDF1) gene.";
 RL Genomics 28:495-500(1995).
 RN [3]
 RP NUCLEOTIDE SEQUENCE (ISOFORM ALPHA).
 RC TISSUE=Liver;
 RA Begun N.A., Barnard G.F.;
 RT "Nucleotide sequence of hIRH, human interleukin reduced in hepatomas.";
 RL Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP NUCLEOTIDE SEQUENCE (GENOMIC DNA).
 RA Rieder M.J., Johanson E.J., da Ponte S.H., Hastings N.C., Ahearn M.O.,
 RA Bertucci C.B., Wong M.W., Yi Q., Nickerson D.A.;
 RT "SeattleSNPs: NHLBI HL6682 program for genomic applications, UW-
 RT FHCR, Seattle, WA (URL: <http://pga.gs.washington.edu>).";
 RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RX PubMed=15164034; DOI=10.1038/nature02462;
 RA Deloukas P., Earthworm M.E., Grafham D.V., Rubenfield M., French L.,
 RA Steward C.A., Sims S.K., Jones M.C., Searle S., Scott C., Howe K.,
 RA Hunt S.E., Andrews T.D., Gilbert J.G.R., Swarbreck D., Ashurst J.L.,
 RA Taylor A., Battles J., Bird C.P., Ainscough R., Almeida J.P.,
 RA Ashwell R.I.S., Ambrose K.D., Babbage A.K., Baggeley C.L., Bailey J.,
 RA Banerjee R., Bates K., Beasley H., Bray-Allen S., Brown A.J.,
 RA Brown J.Y., Burford D.C., Burrill W., Burton J., Cahill P., Camire D.,
 RA Carter N.P., Chapman J.C., Clark S.Y., Clarke G., Clee C.M., Clegg S.,
 RA Corby N., Coulson A., Dhani P., Dutta I., Dunn M., Faulkner L.,
 RA Frankish A., Frankland J.A., Garner P., Garnett J., Gribble S.,

Griffiths C., Grocock R., Gustafson E., Hammond S., Harley J.L.,
 Hart E., Heath P.D., Ho T.P., Hopkins B., Horne J., Howden P.J.,
 RA Huckle E., Hynds C., Johnson C., Johnson D., Kana A., Kay M.,
 RA Kimberley A.M., Kersey J.K., Kokkinaki M., Laird G.K., Lawlor S.,
 RA Lee H.M., Leongamornlert D.A., Laird G., Lloyd C., Lloyd D.M.,
 RA Loveland J., Lovell J., McLaren S., McLay K.E., McMurray A.,
 RA Mashregi-Mohammadi M., Matthews L., Milne S., Nickerson T.,
 RA Nguyen M., Overton-Latty E., Palmer S.A., Pearce A.V., Peck A.I.,
 RA Pelan S., Phillimore B., Porter K., Rice C.M., Rogosin A., Ross M.T.,
 RA Sarafidou T., Sehra H.K., Showkhen R., Skuce C.D., Smith M.,
 RA Standing L., Sycamore N., Tester J., Thorpe A., Torcaso W.,
 RA Tracey A., Tromans A., Tsolas J., Wall M., Walsh J., Wang H.,
 RA Weinstock K., West A.P., Willey D.L., Whitehead S.L., Wilming L.,
 RA Wray P.W., Young L., Chen Y., Lovering R.C., Moschonas N.K.,
 RA Siebert R., Fechtel K., Bentley D., Durbin R., Hubbard T.,
 RA Doucette-Stamm L., Beck S., Smith D.R., Rogers J.;
 RT "The DNA sequence and comparative analysis of human chromosome 10.";
 RL Nature 429:375-381(2004).
 RN [6]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM ALPHA).
 RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Guaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyar S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Scherf A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [7]
 RP IDENTIFICATION OF SDF-1ALPHA(3-67) AND SDF-1BETA(3-72) BY MASS
 RP SPECTROMETRY, AND N-TERMINAL AND C-TERMINAL PROCESSING.
 RX PubMed=14525775; DOI=10.1182/blood-2003-08-2857;
 RA De La Luz Sierra M., Yang F., Narazaki M., Salvucci O., Davis D.,
 RA Yarchoan R., Zhang H.H., Fales H., Tosato G.;
 RT "Differential processing of stromal-derived factor-lalpha and beta
 RT explains functional diversity.";
 RL Blood 103:2452-2459(2004).
 RN [8]
 RP STRUCTURE BY NMR OF 22-88.
 RX MEDLINE=98046030; PubMed=9384579; DOI=10.1093/emboj/16.23.6996;
 RA Crump M.P., Gong J.H., Loetscher P., Rajaratnam K., Amara A.,
 RA Arenzana-Seisdedos F., Virelizier J.L., Baggiolini M., Sykes B.D.,
 RA Clark-Lewis I.;
 RT "Solution structure and basis for functional activity of stromal cell-
 RT derived factor-1; dissociation of CXCR4 activation from binding and
 RT inhibition of HIV-1.";
 RL EMBO J. 16:6996-7007(1997).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 22-88.
 RX MEDLINE=98284037; PubMed=9618518; DOI=10.1073/pnas.95.12.6941;
 RA Dealwis C., Fernandez E.J., Thompson D.A., Simon R.J., Siani M.A.,
 RA Lolis E.;
 RT "Crystal structure of chemically synthesized [N3A] stromal cell-
 RT derived factor 1alpha, a potent ligand for the HIV-1 'fusin'
 RT coreceptor.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:6941-6946(1998).
 CC -!- FUNCTION: Chemoattractant active on T-lymphocytes, monocytes, but
 CC not neutrophils. SDF-1-beta(3-72) and SDF-1-alpha(3-67) show a
 CC reduced chemotactic activity. Binding to cell surface

```

CC proteoglycans seems to inhibit formation of SDF-1-alpha(3-67) and
CC thus to preserve activity on local sites.
CC -!- SURCELLULAR LOCATION: Secreted protein.
CC -!- ALTERNATIVE PRODUCTS:
CC   Event=Alternative splicing; Named isoforms=2;
CC   Name=Beta; Synonyms=SDF-1-beta(1-72);
CC   IsoId=P48061-1; Sequences=Displayed;
CC   Name=Alpha; Synonyms=SDF-1-alpha(1-68);
CC   IsoId=P48061-2; Sequences=VSP_001056;
CC -!- PTM: Processed forms SDF-1-beta(3-72) and SDF-1-alpha(3-67) are
CC produced after secretion by proteolytic cleavage of isoforms Beta
CC and Alpha, respectively. The N-terminal processing is probably
CC achieved by DP4. Isoform Alpha is first cleaved at the C-terminus
CC to yield a SDF-1-alpha(1-67) intermediate before being processed
CC at the N-terminus. The C-terminal processing of isoform Alpha is
CC reduced by binding to heparin and, probably, cell surface
CC proteoglycans.
CC -!- SIMILARITY: Belongs to the intercrine alpha (chemokine Cx)
CC family.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; U16752; AAA97434.1; -; mRNA.
DR EMBL; L36033; AAB39332.1; -; mRNA.
DR EMBL; L36034; AAB39333.1; -; mRNA.
DR EMBL; U19495; AAB40516.1; -; mRNA.
DR EMBL; AY802782; AAV49999.1; -; Genomic DNA.
DR EMBL; AL137026; CAC10203.1; -; Genomic DNA.
DR EMBL; BC039893; AAB39893.1; -; mRNA.
DR PIR; G01540; G01540.
DR PDB; 1A15; X-ray; A/B=22-88.
DR PDB; 1OG7; X-ray; A/B=22-88.
DR PDB; 1SGF; NMR; @=22-88.
DR PDB; 1VMC; NMR; A=19-89.
DR PDB; 2SDF; NMR; @=22-88.
DR Ensembl; ENSG00000107562; Homo sapiens.
DR HGNC; HGNC:10672; CXCL12.
DR MIM; 600835; gene.
DR LinkHub; P48061; -.
DR GO; GO:0008009; F:chemokine activity; TAS.
DR GO; GO:0005102; F:receptor binding; TAS.
DR GO; GO:0006874; P:calcium ion homeostasis; TAS.
DR GO; GO:0007155; P:cell adhesion; TAS.
DR GO; GO:0006935; P:chemotaxis; TAS.
DR GO; GO:0008015; P:circulation; TAS.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.
DR GO; GO:0006955; P:immune response; TAS.
DR GO; GO:0008064; P:regulation of actin polymerization and/or d. . .; TAS.
DR GO; GO:0009615; P:response to virus; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.
DR InterPro; IPR002473; C-X-C/interlkn_8.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR PRINTS; PR00436; INTERLEUKIN8.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00471; SMALL_CYTOKINES_CXC; FALSE NEG.
KW 3D-structure; Alternative splicing; Chemotaxis; Cytokine;
KW Growth factor; Sensory transduction; Signal.
FT SIGNAL 1 21 Potential.
FT CHAIN 22 93 Stromal cell-derived factor 1.
FT CHAIN 24 93 SDF-1-beta(3-72).
FT CHAIN 24 98 /FTID=PRO_0000005110.
FT DISULFID 30 55 SDF-1-alpha(3-67).
FT DISULFID 32 71 /FTID=PRO_0000005111.
FT VARSPLIC 90 93 Missing (in isoform Alpha).
FT STRAND 31 31 /FTID=VSP_001056.
FT STRAND 33 34

```

```

FT STRAND 36 36
FT HELIX 41 43

Query Match 100.0%; Score 28; DB 1; Length 93;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLSYR 6
Db 24 VLSYR 29
|||||

RESULT 12
Q3LSL4 CANFA
ID Q3LSL4_CANFA PRELIMINARY; PRT; 93 AA.
AC Q3LSL4;
DT 25-OCT-2005, integrated into UniProtKB/TrEMBL.
DT 25-OCT-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Chemokine (C-X-C motif) ligand 12 isoform beta.
GN Name=CXCL12;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Tsuchida S., Kagi A., Takahashi T.;
RT "Evaluation of the canine CXCR4 and CXCL12 genes as a candidate for
RT chronic neutropenia with myelokathexis in a border collie dog.";
RL Submitted (AUG-2005) to the EMBL/GenBank/DBJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; DQ182701; ABA28311.1; -; mRNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0008009; F:chemokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR002473; C-X-C/interlkn_8.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR PRINTS; PR00436; INTERLEUKIN8.
DR SMART; SM00199; SCY; 1.
DR SEQUENCE 93 AA; 10591 MW; 004B6AD271F8D2D6 CRC64;

Query Match 100.0%; Score 28; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLSYR 6
Db 24 VLSYR 29
|||||

RESULT 13
QSR8M6_PONPY
ID QSR8M6_PONPY PRELIMINARY; PRT; 93 AA.
AC QSR8M6;
DT 21-DEC-2004, integrated into UniProtKB/TrEMBL.
DT 21-DEC-2004, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Hypothetical protein DKFP469G1525.
GN Name=DKFP469G1525;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;

```

RG The German CDNA Consortium;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RA Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL: CR859725; CAH91884.1; -; mRNA.
DR SNR; QSRM6; 23-88.
DR GO; GO:000576; C:extracellular region; IEA.
DR GO; GO:0008009; F:chemokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR002473; C-X-C/Interlkn_8.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR PRINTS; PR00436; INTERLEUKIN8.
DR SMART; SM00199; SCY; 1.
KW Hypothetical protein.
SQ SEQUENCE 93 AA; 10655 MW; 551D6828FF9183D CRC64;

Query Match 100.0%; Score 28; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. NO. 75;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSLSYR 6
Db 24 VSLSYR 29

RESULT 14
Q4FUL5 MOUSE
ID Q4FUL5 MOUSE PRELIMINARY; PRT; 93 AA.
AC Q4FUL5;
DT 30-AUG-2005, integrated into UniProtKB/TrEMBL.
DT 30-AUG-2005, sequence version 1.
DE 07-FEB-2006, entry version 6.
DE Cxcl12 protein (Activated spleen cDNA, RIKEN full-length enriched
DE library, clone: F830223B13 product: chemokine (C-X-C motif) ligand 12,
DE full insert sequence).
DE DE Names: Cxcl12;
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP Nucleotide SEQUENCE.
RA Ebert L., Muenstermann E., Schatten R., Henze S., Bohn E.,
RA Mollenhauer J., Wiemann S., Schick M., Korn B.;
RA "Cloning of mouse full open reading frames in Gateway(R) system entry
RA vector (pDONR201).";
RA Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP Nucleotide SEQUENCE.
RC STRAIN=NOD; TISSUE=Activated spleen;
RX MEDLINE=16141072; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Methods Enzymol. 303:19-44(1999).
RN [3]
RP Nucleotide SEQUENCE.
RC STRAIN=NOD; TISSUE=Activated spleen;
RX PubMed=16141072; DOI=10.1126/science.1112014;
RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA Ambesi-Impombato A., Apweiler R., Attalini R.N., Bailey T.L.,
RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,

RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA Hill D., Huminteki L., Iacono M., Ikeo K., Iwano A., Ishikawa T.,
RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA Mottagui-Tabar S., Mulder N., Nakano N., Nakamura H., Ng P.,
RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
RA Petrovsky N., Piazza S., Reed J., Reid J.P., Ring B.Z., Ringwald M.,
RA Rost B., Ruan Y., Salzberg S.L., Sanderlin A., Schneider C.,
RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA Sperling S., Stupka E., Sugimura K., Sultana R., Takenaka Y., Taki K.,
RA Tamboja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Nimmiya N.,
RA Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,
RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA Hayashizaki Y.;
RT "The transcriptional landscape of the mammalian genome.";
RL Science 309:1559-1563(2005).
RN [4]
RP Nucleotide SEQUENCE.
RC STRAIN=NOD; TISSUE=Activated spleen;
RX PubMed=16141073; DOI=10.1126/science.1112009;
RA RIKEN Genome Exploration Research Group, and Genome Science Group
RA (Genome Network Core Team) and the FANTOM Consortium;
RT "Antisense Transcription in the Mammalian Transcriptome.";
RL Science 309:1564-1566(2005).
RN [5]
RP Nucleotide SEQUENCE.
RC STRAIN=NOD; TISSUE=Activated spleen;
RX MEDLINE=22546681; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusci V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.P., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sanderlin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayaseu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Miyazaki A., Sakai K., Sasaki D., Ishii Y., Itoh M., Kagawa I.,
RA Yamanishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [6]
RP Nucleotide SEQUENCE.

```
RC STRAIN=NOD; TISSUE=Activated spleen;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gofjoberi T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Mateuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fletschmann W., Gaasterland T., Glasi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald W., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [7]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOD; TISSUE=Activated spleen;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [8]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOD; TISSUE=Activated spleen;
RX MEDLINE=20350913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [9]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOD; TISSUE=Activated spleen;
RA Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
RA Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
RA Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
RA Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
-----
DR EMBL; CT010389; CAJ18596.1; -; mRNA.
DR EMBL; AK157553; BAE34120.1; -; mRNA.
DR SMR; Q4FJL5; 23-88.
DR MGI; MGI:103556; Cxcl12.
DR GO; GO:0005615; C:extracellular space; RCA.
DR GO; GO:0008009; P:chemokine activity; IDA.
DR GO; GO:0001667; P:ameboid cell migration; IMP.
DR GO; GO:0007420; P:brain development; IDA.
DR GO; GO:0007281; P:germ cell development; IDA.
DR GO; GO:0008354; P:germ cell migration; IDA.
DR GO; GO:0005030; P:induction of positive chemotaxis; IDA.
DR GO; GO:0001569; P:patterning of blood vessels; IMP.
DR GO; GO:0030335; P:positive regulation of cell migration; IDA.
DR GO; GO:0042098; P:T cell proliferation; IMP.
```

```
DR InterPro; IPR002473; C-X-C/Interlkn_8.
DR InterPro; IPR001811; Chemokine_IL8_.
DR Pfam; PF00048; IL8; 1.
DR PRINTS; PR00436; INTERLEUKIN8.
DR SMART; SM00199; SCY; 1.
SQ SEQUENCE 93 AA; 10561 MW; 625367D344B8AD69 CRC64;

Query Match 100.0%; Score 28; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLSYR 6
| | | | |
Db 24 VLSYR 29

RESULT 15
Q2L985 HUMAN PRELIMINARY; PRT; 100 AA.
AC Q2L985;
DT 21-FEB-2006, integrated into UniProtKB/TrEMBL.
DT 21-FEB-2006, sequence version 1.
DT 21-FEB-2006, entry version 1.
DE Stromal cell-derived factor 1 theta.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Yu L., Cecil J., Peng S.-B., Schrementia J., Kovacevic S., Paul D.,
RA Su E.W., Wang J.;
RT "Identification and expression of novel isoforms of human stromal
cell-derived factor 1.";
RL Submitted (DEC-2005) to the EMBL/GenBank/DBJ databases.
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
-----
DR EMBL; DQ345520; ABC69273.1; -; mRNA.
SQ SEQUENCE 100 AA; 11395 MW; BFF2739B8E70BAAD CRC64;

Query Match 100.0%; Score 28; DB 2; Length 100;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLSYR 6
| | | | |
Db 24 VLSYR 29

Search completed: August 10, 2006, 23:10:00
Job time : 102 secs
```


GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 10, 2006, 23:13:31 ; Search time 16.3636 Seconds
(without alignments)
37.022 Million cell updates/sec

Title: US-10-825-603-2

Perfect score: 33

Sequence: 1 RXVSLSYRX 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 239914 seqs, 67312017 residues

Total number of hits satisfying chosen parameters: 239914

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New.*
1: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	-28	84.8	93	6 US-10-505-928-112	Sequence 112, App
2	28	84.8	93	6 US-10-511-937-2454	Sequence 2454, App
3	28	84.8	168	6 US-10-449-902-55009	Sequence 55009, A
4	28	84.8	607	6 US-10-449-902-47399	Sequence 47399, A
5	27	81.8	372	7 US-11-056-355B-81312	Sequence 81312, A
6	27	81.8	439	7 US-11-056-355B-81311	Sequence 81311, A
7	27	81.8	441	7 US-11-056-355B-81310	Sequence 81310, A
8	27	81.8	599	6 US-10-449-902-44762	Sequence 44762, A
9	26	78.8	189	7 US-11-056-355B-27846	Sequence 27846, A
10	26	78.8	189	7 US-11-056-355B-31436	Sequence 31436, A
11	26	78.8	276	7 US-11-056-355B-105356	Sequence 105356, A
12	26	78.8	276	7 US-11-056-355B-116595	Sequence 116595, A
13	26	78.8	277	7 US-11-056-355B-105355	Sequence 105355, A
14	26	78.8	277	7 US-11-056-355B-116594	Sequence 116594, A
15	26	78.8	287	6 US-10-953-349-4876	Sequence 4876, App
16	26	78.8	302	6 US-10-953-349-4875	Sequence 4875, App
17	26	78.8	306	7 US-11-056-355B-105354	Sequence 105354, A
18	26	78.8	306	7 US-11-056-355B-116593	Sequence 116593, A
19	26	78.8	314	6 US-10-953-349-5664	Sequence 5664, App
20	26	78.8	314	7 US-11-056-355B-28620	Sequence 28620, A
21	26	78.8	314	7 US-11-056-355B-37631	Sequence 37631, A
22	26	78.8	315	6 US-10-953-349-5663	Sequence 5663, App
23	26	78.8	315	7 US-11-056-355B-26619	Sequence 26619, A
24	26	78.8	315	7 US-11-056-355B-37630	Sequence 37630, A
25	26	78.8	337	7 US-11-056-355B-47394	Sequence 47394, A

26	78.8	344	6 US-10-953-349-5662	Sequence 5662, App
26	78.8	344	7 US-11-056-355B-28618	Sequence 28618, A
28	78.8	344	7 US-11-056-355B-37629	Sequence 37629, A
29	78.8	532	7 US-11-056-355B-47393	Sequence 47393, A
30	78.8	543	7 US-11-056-355B-47392	Sequence 47392, A
31	78.8	556	6 US-10-449-902-55969	Sequence 55969, A
32	78.8	608	6 US-10-449-902-55390	Sequence 55390, A
33	78.8	163	6 US-10-449-902-29776	Sequence 29776, A
34	75.8	163	6 US-10-449-902-50928	Sequence 50928, A
35	75.8	170	6 US-10-953-349-26849	Sequence 26849, A
36	75.8	206	6 US-10-953-349-31407	Sequence 31407, A
37	75.8	255	6 US-10-953-349-31408	Sequence 31408, A
38	75.8	256	6 US-10-953-349-19900	Sequence 19900, A
39	75.8	267	6 US-10-953-349-25239	Sequence 25239, A
40	75.8	267	7 US-11-056-355B-57120	Sequence 57120, A
41	75.8	300	6 US-10-953-349-19899	Sequence 19899, A
42	75.8	301	7 US-11-056-355B-53929	Sequence 53929, A
43	75.8	311	6 US-10-953-349-25238	Sequence 25238, A
44	75.8	311	7 US-11-056-355B-57119	Sequence 57119, A
45	75.8	324	6 US-10-953-349-31406	Sequence 31406, A

ALIGNMENTS

RESULT 1
US-10-505-928-112
; Sequence 112, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; PRIOR FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 112
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-112

Query Match 84.8%; Score 28; DB 6; Length 93;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 VLSYR 8
|||
DB 24 VLSYR 29

RESULT 2
US-10-511-937-2454
; Sequence 2454, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; PRIOR FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946

; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2454
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-937-2454

Query Match 84.8%; Score 28; DB 6; Length 93;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 VLSYR 8
Db 24 VLSYR 29

RESULT 3

US-10-449-902-55009
; Sequence 55009, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-Oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205V1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55009
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-55009

Query Match 84.8%; Score 28; DB 6; Length 168;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 VLSYR 8
Db 73 VLSYR 78

RESULT 4

US-10-449-902-47399
; Sequence 47399, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-Oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205V1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11

; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47399
; LENGTH: 607
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-47399

Query Match 84.8%; Score 28; DB 6; Length 607;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 VLSYR 8
Db 73 VLSYR 78

RESULT 5

US-11-056-355B-81312
; Sequence 81312, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 81312
; LENGTH: 372
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(372)
; OTHER INFORMATION: Ceres Seq. ID no. 12659264
US-11-056-355B-81312

Query Match 81.8%; Score 27; DB 7; Length 372;
Best Local Similarity 62.5%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RXVLSYR 8
Db 318 RSVSISYQ 325

RESULT 6

US-11-056-355B-81311
; Sequence 81311, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 81311
; LENGTH: 439
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(439)

OTHER INFORMATION: Ceres Seq. ID no. 12659263
US-11-056-355B-81311

Query Match 81.8%; Score 27; DB 7; Length 439;
Best Local Similarity 62.5%; Pred. No. 1.4e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RXVSLSYR 8
| : : : :
Db 385 RSVSISYQ 392

RESULT 7

US-11-056-355B-81310
; Sequence 81310, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 81310
; LENGTH: 441
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(441)
; OTHER INFORMATION: Ceres Seq. ID no. 12659262
US-11-056-355B-81310

Query Match 81.8%; Score 27; DB 7; Length 441;
Best Local Similarity 62.5%; Pred. No. 1.4e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RXVSLSYR 8
| : : : :
Db 387 RSVSISYQ 394

RESULT 8

US-10-449-902-44762
; Sequence 44762, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44762
; LENGTH: 599
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-44762

Query Match 81.8%; Score 27; DB 6; Length 599;
Best Local Similarity 62.5%; Pred. No. 1.9e+02;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 RXVSLSYR 8
| : : : :
Db 51 RTLALSYR 58

RESULT 9

US-11-056-355B-27846
; Sequence 27846, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 27846
; LENGTH: 189
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(189)
; OTHER INFORMATION: Ceres Seq. ID no. 12340194
US-11-056-355B-27846

Query Match 78.8%; Score 26; DB 7; Length 189;
Best Local Similarity 71.4%; Pred. No. 99;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RXVSLSY 7
| : : : :
Db 50 RDISLSY 56

RESULT 10

US-11-056-355B-31436
; Sequence 31436, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 31436
; LENGTH: 189
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(189)
; OTHER INFORMATION: Ceres Seq. ID no. 12340194
US-11-056-355B-31436

Query Match 78.8%; Score 26; DB 7; Length 189;
Best Local Similarity 71.4%; Pred. No. 99;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RXVSLSY 7
| : : : :
Db 50 RDISLSY 56

```
RESULT 11
US-11-056-355B-105356
; Publication No. US20060150283A1
; Sequence 105356, Application US/11056355B
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 105356
; LENGTH: 276
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(276)
; OTHER INFORMATION: Ceres Seq. ID no. 13617049
US-11-056-355B-105356

Query Match      78.8%; Score 26; DB 7; Length 276;
Best Local Similarity 71.4%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RXVSLSY 7
Db 175 RDLSLSY 181

RESULT 12
US-11-056-355B-116595
; Sequence 116595, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 116595
; LENGTH: 276
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(276)
; OTHER INFORMATION: Ceres Seq. ID no. 13617049
US-11-056-355B-116595

Query Match      78.8%; Score 26; DB 7; Length 276;
Best Local Similarity 71.4%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RXVSLSY 7
Db 175 RDLSLSY 181

RESULT 13
US-11-056-355B-105355
; Sequence 105355, Application US/11056355B
```

```
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 105355
; LENGTH: 277
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(277)
; OTHER INFORMATION: Ceres Seq. ID no. 13617048
US-11-056-355B-105355

Query Match      78.8%; Score 26; DB 7; Length 277;
Best Local Similarity 71.4%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RXVSLSY 7
Db 176 RDLSLSY 182

RESULT 14
US-11-056-355B-116594
; Sequence 116594, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 116594
; LENGTH: 277
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(277)
; OTHER INFORMATION: Ceres Seq. ID no. 13617048
US-11-056-355B-116594

Query Match      78.8%; Score 26; DB 7; Length 277;
Best Local Similarity 71.4%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RXVSLSY 7
Db 176 RDLSLSY 182

RESULT 15
US-10-953-349-4876
; Sequence 4876, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
```

```

; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4876
; LENGTH: 287
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-4876

Query Match      78.8%; Score 26; DB 6; Length 287;
Best Local Similarity 62.5%; Pred. No. 1.5e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 RXVSLSYR 8
Db      41 RRVALTYR 48

Search completed: August 10, 2006, 23:20:42
Job time : 17.3636 secs

```

THIS PAGE BLANK (USPTO)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 10, 2006, 23:11:26 ; Search time 103.636 Seconds
(without alignments)
40.227 Million cell updates/sec

Title: US-10-825-603-2

Perfect score: 33

Sequence: 1 RXVSLSYRX 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	100.0	9	5	US-10-825-603-1
2	33	100.0	9	5	US-10-825-603-5
3	32	97.0	9	5	US-10-825-603-2
4	31	93.9	94	4	US-10-437-963-161946
5	30	90.9	863	4	US-10-282-122A-76464
6	30	90.9	863	5	US-10-732-923-18292
7	29	87.9	8	3	US-09-852-424-131
8	29	87.9	9	3	US-09-852-424-14
9	29	87.9	9	3	US-09-852-424-15
10	29	87.9	9	3	US-09-852-424-16
11	29	87.9	9	3	US-09-852-424-130
12	29	87.9	9	3	US-09-852-424-132
13	29	87.9	9	5	US-10-945-674A-14
14	29	87.9	9	5	US-10-945-674A-15
15	29	87.9	9	5	US-10-945-674A-16
16	29	87.9	9	5	US-10-945-674A-134
17	29	87.9	9	5	US-10-945-674A-136
18	29	87.9	9	6	US-11-060-031-2
19	29	87.9	9	6	US-11-060-031-3
20	29	87.9	9	6	US-11-136-097-2
21	29	87.9	9	6	US-11-136-097-3
22	29	87.9	10	6	US-11-060-031-4
23	29	87.9	10	6	US-11-136-097-4
24	29	87.9	14	5	US-10-945-674A-76
25	29	87.9	14	5	US-10-945-674A-128
26	29	87.9	14	5	US-10-945-674A-131
27	29	87.9	17	3	US-09-852-424-13

28	29	87.9	17	5	US-10-945-674A-13	Sequence 13, Appl
29	29	87.9	17	5	US-10-945-674A-78	Sequence 78, Appl
30	29	87.9	28	3	US-09-852-424-76	Sequence 76, Appl
31	29	87.9	30	3	US-09-852-424-127	Sequence 127, App
32	29	87.9	30	3	US-09-852-424-129	Sequence 129, App
33	29	87.9	31	3	US-09-852-424-74	Sequence 74, Appl
34	29	87.9	31	3	US-09-852-424-77	Sequence 77, Appl
35	29	87.9	31	3	US-09-852-424-122	Sequence 122, App
36	29	87.9	31	3	US-09-852-424-124	Sequence 124, App
37	29	87.9	31	3	US-09-852-424-133	Sequence 133, App
38	29	87.9	31	3	US-09-852-424-134	Sequence 134, App
39	29	87.9	31	3	US-09-852-424-135	Sequence 135, App
40	29	87.9	31	5	US-10-222-703A-11	Sequence 11, Appl
41	29	87.9	31	5	US-10-222-703A-20	Sequence 20, Appl
42	29	87.9	31	5	US-10-222-703A-29	Sequence 29, Appl
43	29	87.9	31	5	US-10-222-703A-38	Sequence 38, Appl
44	29	87.9	31	5	US-10-222-703A-308	Sequence 308, App
45	29	87.9	31	5	US-10-222-703A-317	Sequence 317, App

ALIGNMENTS

RESULT 1

US-10-825-603-1
; Sequence 1, Application US/10825603
; Publication No. US20050042635A1
; GENERAL INFORMATION:
; APPLICANT: THACKER, JAMES D.
; APPLICANT: FUHRER, PETER J.
; APPLICANT: WILLEFORD, KENNETH O.
; TITLE OF INVENTION: PROPHYLACTIC AND THERAPEUTIC BENEFITS OF A NEW CLASS OF
; FILE REFERENCE: IMMUNE STIMULATING PEPTIDES
; FILE REFERENCE: 54442-20005.00
; CURRENT APPLICATION NUMBER: US/10/825,603
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 60/463,042
; PRIOR FILING DATE: 2003-04-16
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; FEATURE:
; OTHER INFORMATION: see specification as filed for preferred embodiments
US-10-825-603-1

Query Match 100.0%; Score 33; DB 5; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.9e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RXVSLSYR 8
| | | | |
Db 1 RSVSLSYR 8

RESULT 2

US-10-825-603-5
; Sequence 5, Application US/10825603
; Publication No. US20050042635A1
; GENERAL INFORMATION:
; APPLICANT: THACKER, JAMES D.
; APPLICANT: FUHRER, PETER J.
; APPLICANT: WILLEFORD, KENNETH O.
; TITLE OF INVENTION: PROPHYLACTIC AND THERAPEUTIC BENEFITS OF A NEW CLASS OF
; FILE REFERENCE: IMMUNE STIMULATING PEPTIDES
; FILE REFERENCE: 54442-20005.00
; CURRENT APPLICATION NUMBER: US/10/825,603
; CURRENT FILING DATE: 2004-04-16

; PRIOR APPLICATION NUMBER: 60/463,042
; PRIOR FILING DATE: 2003-04-16
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 5

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-825-603-5

Query Match 100.0%; Score 33; DB 5; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.9e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RXVSLSYR 8
| | | | |
Db 1 RSVLSYR 8

RESULT 3

US-10-825-603-2
; Sequence 2, Application US/10825603
; Publication No. US20050042635A1
; GENERAL INFORMATION:
; APPLICANT: THACKER, JAMES D.
; APPLICANT: FUHRER, PETER J.
; APPLICANT: WILLEFORD, KENNETH O.
; TITLE OF INVENTION: PROPHYLACTIC AND THERAPEUTIC BENEFITS OF A NEW CLASS OF
; TITLE OF INVENTION: IMMUNE STIMULATING PEPTIDES
; FILE REFERENCE: 54442-20005.00
; CURRENT APPLICATION NUMBER: US/10/825,603
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 60/463,042
; PRIOR FILING DATE: 2003-04-16
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (2)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (9)
; OTHER INFORMATION: Variable amino acid
US-10-825-603-2

Query Match 97.0%; Score 32; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXVSLSYR 8
| | | | |
Db 1 RSVLSYR 8

RESULT 4

US-10-437-963-161946
; Sequence 161946, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 161946
; LENGTH: 94
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_61084C.1.pcp
US-10-437-963-161946

Query Match 93.9%; Score 31; DB 4; Length 94;
Best Local Similarity 87.5%; Pred. No. 47;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RXVLSYR 8
| | | | |
Db 51 RWVLSYR 58

RESULT 5

US-10-282-122A-76464
; Sequence 76464, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 76464


```
; LENGTH: 863
; TYPE: PRT
; ORGANISM: Treponema pallidum
US-10-282-122A-76464

Query Match          90.9%; Score 30; DB 4; Length 863;
Best Local Similarity 75.0%; Pred. No. 7.5e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RXVSLSYR 8
Db 135 RTVALSYR 142

RESULT 6
US-10-732-923-18292
; Sequence 18292, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 80021-257
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 18292
; LENGTH: 863
; TYPE: PRT
; ORGANISM: Treponema pallidum
US-10-732-923-18292

Query Match          90.9%; Score 30; DB 5; Length 863;
Best Local Similarity 75.0%; Pred. No. 7.5e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RXVSLSYR 8
Db 135 RTVALSYR 142

US-09-852-424-131
; Sequence 131, Application US/09852424
; Patent No. US20020156034A1
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia; and
; APPLICANT: Chemokine Therapeutics Corporation
; TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS
; FILE REFERENCE: 80021-257
; CURRENT APPLICATION NUMBER: US/09/852,424
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: CA 2,305,787
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 60/205,467
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 131
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (8)
; OTHER INFORMATION: Binds to the residue at position 9 on SEQ ID NO
; OTHER INFORMATION: 130.
; OTHER INFORMATION: Description of Artificial Sequence: Engineered in
; OTHER INFORMATION: Laboratory
US-09-852-424-131

Query Match          87.9%; Score 29; DB 3; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.9e+06;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RXVSLSYR 8
Db 1 KGVSLSYR 8

US-09-852-424-14
; Sequence 14, Application US/09852424
; Patent No. US20020156034A1
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia; and
; APPLICANT: Chemokine Therapeutics Corporation
; TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS
; FILE REFERENCE: 80021-257
; CURRENT APPLICATION NUMBER: US/09/852,424
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: CA 2,305,787
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 60/205,467
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Engineered in
; OTHER INFORMATION: Laboratory
US-09-852-424-14

Query Match          87.9%; Score 29; DB 3; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.9e+06;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RXVSLSYR 8
Db 1 KGVSLSYR 8

US-09-852-424-15
; Sequence 15, Application US/09852424
; Patent No. US20020156034A1
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia; and
; APPLICANT: Chemokine Therapeutics Corporation
; TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS
; FILE REFERENCE: 80021-257
; CURRENT APPLICATION NUMBER: US/09/852,424
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: CA 2,305,787
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 60/205,467
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (9)
; OTHER INFORMATION: dimer of amino acids 1-9 in which the amino acid
; OTHER INFORMATION: chains are joined by a disulphide bond between
; OTHER INFORMATION: each of the cysteines at position 9 in each
; OTHER INFORMATION: sequence.
; OTHER INFORMATION: Description of Artificial Sequence: Engineered in
; OTHER INFORMATION: Laboratory (SDF-1 (1-9)2 [P2G])
US-09-852-424-15
```

US-09-852-424-15

Query Match 87.9%; Score 29; DB 3; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.9e+06;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 RXVSLSYR 8
: |||||
Db 1 KGVSLSYR 8

RESULT 10

US-09-852-424-16
; Sequence 16, Application US/09852424
; Patent No. US20020156034A1
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia; and
; APPLICANT: Chemokine Therapeutics Corporation
; TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS
; FILE REFERENCE: 80021-257
; CURRENT APPLICATION NUMBER: US/09/852,424
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: CA 2,305,787
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 60/205,467
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (9)
; OTHER INFORMATION: Xaa-an amino acid like lysine; ornithine or any
; OTHER INFORMATION: other natural or unnatural amino acid serving as a
; OTHER INFORMATION: linker between each of the arginines at position 8
; OTHER INFORMATION: in each of SEQ ID NOS 16 and 17.
; OTHER INFORMATION: Description of Artificial Sequence: Engineered in
; OTHER INFORMATION: Laboratory (SDF-1(1-8)2[P2G])
US-09-852-424-16

Query Match 87.9%; Score 29; DB 3; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.9e+06;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RXVSLSYR 8
: |||||
Db 1 KGVSLSYR 8

RESULT 11

US-09-852-424-130
; Sequence 130, Application US/09852424
; Patent No. US20020156034A1
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia; and
; APPLICANT: Chemokine Therapeutics Corporation
; TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS
; FILE REFERENCE: 80021-257
; CURRENT APPLICATION NUMBER: US/09/852,424
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: CA 2,305,787
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 60/205,467
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 130
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence

; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (9)_
; OTHER INFORMATION: AMIDATION; acts as a linking moiety between each
; OTHER INFORMATION: arginine at position 8 in each of SEQ ID 130 and
; OTHER INFORMATION: SED ID 131.
; OTHER INFORMATION: Description of Artificial Sequence: Engineered in
; OTHER INFORMATION: Laboratory
US-09-852-424-130

Query Match 87.9%; Score 29; DB 3; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.9e+06;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RXVSLSYR 8
: |||||
Db 1 KGVSLSYR 8

RESULT 12

US-09-852-424-132
; Sequence 132, Application US/09852424
; Patent No. US20020156034A1
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia; and
; APPLICANT: Chemokine Therapeutics Corporation
; TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS
; FILE REFERENCE: 80021-257
; CURRENT APPLICATION NUMBER: US/09/852,424
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: CA 2,305,787
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 60/205,467
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 132
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (9)_
; OTHER INFORMATION: AMIDATION
; OTHER INFORMATION: Description of Artificial Sequence: Engineered in
; OTHER INFORMATION: Laboratory
; NAME/KEY: DISULFID
; LOCATION: (9)
; OTHER INFORMATION: dimer of amino acids 1-9 in which the amino acid
; OTHER INFORMATION: chains are joined by a disulphide bond between
; OTHER INFORMATION: each of the amidated cysteines at position 9 in
; OTHER INFORMATION: each sequence.
US-09-852-424-132

Query Match 87.9%; Score 29; DB 3; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.9e+06;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RXVSLSYR 8
: |||||
Db 1 KGVSLSYR 8

RESULT 13

US-10-945-674A-14
; Sequence 14, Application US/10945674A
; Publication No. US20060014682A1
; GENERAL INFORMATION:
; APPLICANT: Tudan, Christopher R.
; APPLICANT: Merzouk, Ahmed
; APPLICANT: Arab, Lakhdar
; APPLICANT: Saxena, Geeta
; APPLICANT: Eaves, Connie J.

```

; OTHER INFORMATION: KGVSPSYRC (SEQ ID NO:15)
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (9)
; OTHER INFORMATION: dimer of amino acids 1-9 in which the amino acid
; OTHER INFORMATION: chains are joined by a disulphide bond between
; OTHER INFORMATION: each of the cysteines at position 9 in each
; OTHER INFORMATION: sequence
US-10-945-674A-15

Query Match      87.9%; Score 29; DB 5; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.9e+06;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0

Qy 1 RXVSLSYR 8
    : |||||
Db 1 KGVSLSYR 8

RESULT 15
US-10-945-674A-16
; Sequence 16, Application US/10945674A
; Publication No. US20060014682A1
; GENERAL INFORMATION:
; APPLICANT: Tudan, Christopher R.
; APPLICANT: Merzouk, Ahmed
; APPLICANT: Arab, Lakhdar
; APPLICANT: Saxena, Geeta
; APPLICANT: Eaves, Connie J.
; APPLICANT: Cashman, Joanne
; APPLICANT: Clark-Lewis, Ian
; APPLICANT: Salari, Hassan
; APPLICANT: Chemokine Therapeutics Corporation
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: CXCR4 Antagonist Treatment of Hematopoietic Cells
; FILE REFERENCE: 080420-0001000S
; CURRENT APPLICATION NUMBER: US/10/945.674A
; CURRENT FILING DATE: 2004-09-20
; PRIOR APPLICATION NUMBER: CA 2,305,787
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 60/205,467
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 09/852,424
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:synthetic
; OTHER INFORMATION: SDF-1 CXCR4 receptor antagonist analogue dimer
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (9)_
; OTHER INFORMATION: Xaa = an amino acid like Lys, ornithine or any
; OTHER INFORMATION: other natural or unnatural amino acid serving as
; OTHER INFORMATION: linker to the Arg at position 8 of KGVSLSYR
; OTHER INFORMATION: (SEQ ID NO:17)
US-10-945-674A-16

Query Match      87.9%; Score 29; DB 5; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.9e+06;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0

Qy 1 RXVSLSYR 8
    : |||||
Db 1 KGVSLSYR 8

Search completed: August 10, 2006, 23:19:36
Job time : 104.636 secs

```

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

QM protein - protein search, using sw model

Run on: August 10, 2006, 23:11:26 ; Search time 103.636 Seconds
(without alignments)
40.227 Million cell updates/sec

Title: US-10-825-603-1

Perfect score: 43

Sequence: 1 RVSLSYRF 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	100.0	9	5	US-10-825-603-1
2	43	100.0	9	5	US-10-825-603-5
3	37	86.0	1356	6	US-11-129-741-2939
4	37	86.0	1356	6	US-11-129-741-2941
5	37	86.0	1356	6	US-11-129-741-2943
6	37	86.0	1356	6	US-11-129-741-2945
7	37	86.0	1356	6	US-11-129-741-2949
8	37	86.0	1356	6	US-11-129-741-2951
9	37	86.0	1356	6	US-11-129-741-4245
10	37	86.0	1362	5	US-10-895-064-420
11	37	86.0	1362	6	US-11-129-741-420
12	35	81.4	14	5	US-10-222-703A-831
13	35	81.4	14	5	US-10-222-703A-833
14	35	81.4	14	5	US-10-222-703A-855
15	35	81.4	14	5	US-10-222-703A-857
16	35	81.4	31	5	US-10-222-703A-830
17	35	81.4	31	5	US-10-222-703A-832
18	35	81.4	31	5	US-10-222-703A-854
19	35	81.4	31	5	US-10-222-703A-856
20	35	81.4	322	6	US-11-079-463-6615
21	34	79.1	55	4	US-10-437-963-188702
22	33	76.7	9	5	US-10-825-603-2
23	32	74.4	14	5	US-10-222-703A-847
24	32	74.4	14	5	US-10-222-703A-849
25	32	74.4	14	5	US-10-222-703A-851
26	32	74.4	14	5	US-10-222-703A-853
27	32	74.4	31	5	US-10-222-703A-846

28	74.4	31	5	US-10-222-703A-848	Sequence 848, App
29	74.4	31	5	US-10-222-703A-850	Sequence 850, App
30	74.4	31	5	US-10-222-703A-852	Sequence 852, App
31	74.4	53	4	US-10-437-963-135133	Sequence 135133, A
32	74.4	271	4	US-10-029-386-13876	Sequence 33876, A
33	74.4	300	4	US-10-364-049-2346	Sequence 2346, Ap
34	74.4	396	4	US-10-094-749-2492	Sequence 2492, Ap
35	74.4	409	5	US-10-739-930-6621	Sequence 6621, Ap
36	74.4	445	4	US-10-104-047-2209	Sequence 2209, Ap
37	74.4	445	6	US-11-072-512-2209	Sequence 2209, Ap
38	74.4	569	4	US-10-115-482-38	Sequence 38, Appli
39	74.4	859	3	US-09-788-657-16	Sequence 16, Appli
40	74.4	859	3	US-09-912-697-4	Sequence 4, Appli
41	74.4	859	3	US-09-760-285-14	Sequence 14, Appli
42	74.4	859	4	US-10-270-839-25	Sequence 25, Appli
43	74.4	859	4	US-10-243-130-5	Sequence 5, Appli
44	74.4	859	4	US-10-371-634-3	Sequence 3, Appli
45	74.4	859	4	US-10-348-074-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-10-825-603-1
; Sequence 1, Application US/10825603
; Publication No. US20050042635A1
; GENERAL INFORMATION:
; APPLICANT: THACKER, JAMES D.
; APPLICANT: FUHRER, PETER J.
; APPLICANT: WILLEFORD, KENNETH O.
; TITLE OF INVENTION: PROPHYLACTIC AND THERAPEUTIC BENEFITS OF A NEW CLASS OF
; FILE REFERENCE: 54442-20005.00
; CURRENT APPLICATION NUMBER: US/10/825,603
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 60/463,042
; PRIOR FILING DATE: 2003-04-16
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; FEATURE:
; OTHER INFORMATION: peptide
; FEATURE:
; OTHER INFORMATION: see specification as filed for preferred embodiments
US-10-825-603-1

Query Match 100.0%; Score 43; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RVSLSYRF 9
| | | | | | | | |
Db 1 RVSLSYRF 9

RESULT 2

US-10-825-603-5
; Sequence 5, Application US/10825603
; Publication No. US20050042635A1
; GENERAL INFORMATION:
; APPLICANT: THACKER, JAMES D.
; APPLICANT: FUHRER, PETER J.
; APPLICANT: WILLEFORD, KENNETH O.
; TITLE OF INVENTION: PROPHYLACTIC AND THERAPEUTIC BENEFITS OF A NEW CLASS OF
; FILE REFERENCE: 54442-20005.00
; CURRENT APPLICATION NUMBER: US/10/825,603
; CURRENT FILING DATE: 2004-04-16

; PRIOR APPLICATION NUMBER: 60/463,042
; PRIOR FILING DATE: 2003-04-16
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 5
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-825-603-5

Query Match 100.0%; Score 43; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSVLSYRF 9
||| |||||
DB 1 RSVLSYRF 9

RESULT 3

US-11-129-741-2939
; Sequence 2939, Application US/11129741
; Publication No. US20060034853A1
; GENERAL INFORMATION:
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: WOO, CHIU YAT PATRICK
; APPLICANT: LAU, KAR PUI SUSANNA
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: POON, LIT MAN
; APPLICANT: PEIRIS, JOSEPH S.M.
; APPLICANT: GUAN, YI
; TITLE OF INVENTION: A NOVEL HUMAN VIRUS CAUSING RESPIRATORY TRACT
; TITLE OF INVENTION: INFECTION AND USES THEREOF
; FILE REFERENCE: V0690.0044
; CURRENT APPLICATION NUMBER: US/11/129,741
; PRIOR FILING DATE: 2005-05-16
; PRIOR APPLICATION NUMBER: 10/895,064
; PRIOR FILING DATE: 2004-07-21
; NUMBER OF SEQ ID NOS: 4257
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2939
; LENGTH: 1356
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-129-741-2939

Query Match 86.0%; Score 37; DB 6; Length 1356;
Best Local Similarity 77.8%; Pred. No. 1.9e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RSVLSYRF 9
||| |||||
DB 760 RSISASYRF 768

RESULT 4

US-11-129-741-2941
; Sequence 2941, Application US/11129741
; Publication No. US20060034853A1
; GENERAL INFORMATION:
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: WOO, CHIU YAT PATRICK
; APPLICANT: LAU, KAR PUI SUSANNA
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: POON, LIT MAN
; APPLICANT: PEIRIS, JOSEPH S.M.
; APPLICANT: GUAN, YI
; TITLE OF INVENTION: A NOVEL HUMAN VIRUS CAUSING RESPIRATORY TRACT
; TITLE OF INVENTION: INFECTION AND USES THEREOF
; FILE REFERENCE: V0690.0044

; CURRENT APPLICATION NUMBER: US/11/129,741
; CURRENT FILING DATE: 2005-05-16
; PRIOR APPLICATION NUMBER: 10/895,064
; PRIOR FILING DATE: 2004-07-21
; NUMBER OF SEQ ID NOS: 4257
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2941
; LENGTH: 1356
; TYPE: PRT
; ORGANISM: Corononavirus-HKUI
US-11-129-741-2941

Query Match 86.0%; Score 37; DB 6; Length 1356;
Best Local Similarity 77.8%; Pred. No. 1.9e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RSVLSYRF 9
||| |||||
DB 760 RSISASYRF 768

RESULT 5

US-11-129-741-2943
; Sequence 2943, Application US/11129741
; Publication No. US20060034853A1
; GENERAL INFORMATION:
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: WOO, CHIU YAT PATRICK
; APPLICANT: LAU, KAR PUI SUSANNA
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: POON, LIT MAN
; APPLICANT: PEIRIS, JOSEPH S.M.
; APPLICANT: GUAN, YI
; TITLE OF INVENTION: A NOVEL HUMAN VIRUS CAUSING RESPIRATORY TRACT
; TITLE OF INVENTION: INFECTION AND USES THEREOF
; FILE REFERENCE: V0690.0044
; CURRENT APPLICATION NUMBER: US/11/129,741
; PRIOR FILING DATE: 2005-05-16
; PRIOR APPLICATION NUMBER: 10/895,064
; PRIOR FILING DATE: 2004-07-21
; NUMBER OF SEQ ID NOS: 4257
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2943
; LENGTH: 1356
; TYPE: PRT
; ORGANISM: Corononavirus-HKUI
US-11-129-741-2943

Query Match 86.0%; Score 37; DB 6; Length 1356;
Best Local Similarity 77.8%; Pred. No. 1.9e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RSVLSYRF 9
||| |||||
DB 760 RSISASYRF 768

RESULT 6

US-11-129-741-2945
; Sequence 2945, Application US/11129741
; Publication No. US20060034853A1
; GENERAL INFORMATION:
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: WOO, CHIU YAT PATRICK
; APPLICANT: LAU, KAR PUI SUSANNA
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: POON, LIT MAN
; APPLICANT: PEIRIS, JOSEPH S.M.
; APPLICANT: GUAN, YI
; TITLE OF INVENTION: A NOVEL HUMAN VIRUS CAUSING RESPIRATORY TRACT
; TITLE OF INVENTION: INFECTION AND USES THEREOF
; FILE REFERENCE: V0690.0044
; CURRENT APPLICATION NUMBER: US/11/129,741

; CURRENT FILING DATE: 2005-05-16
; PRIOR APPLICATION NUMBER: 10/895,064
; PRIOR FILING DATE: 2004-07-21
; NUMBER OF SEQ ID NOS: 4257
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2945
; LENGTH: 1356
; TYPE: PRT
; ORGANISM: Corononavirus-HKU1
US-11-129-741-2945

Query Match 86.0%; Score 37; DB 6; Length 1356;
Best Local Similarity 77.8%; Pred. No. 1.9e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RSVSLSYRF 9
||:|||||
Db 760 RSISASYRF 768

RESULT 7

US-11-129-741-2949
; Sequence 2949, Application US/11129741
; Publication No. US20060034853A1
; GENERAL INFORMATION:
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: WOO, CHIU YAT PATRICK
; APPLICANT: LAU, KAR PUI SUSANNA
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: POON, LIT MAN
; APPLICANT: PEIRIS, JOSEPH S.M.
; APPLICANT: GUAN, YI
; TITLE OF INVENTION: A NOVEL HUMAN VIRUS CAUSING RESPIRATORY TRACT
; FILE REFERENCE: V0690.0044
; CURRENT APPLICATION NUMBER: US/11/129,741
; PRIOR FILING DATE: 2005-05-16
; PRIOR APPLICATION NUMBER: 10/895,064
; PRIOR FILING DATE: 2004-07-21
; NUMBER OF SEQ ID NOS: 4257
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2949
; LENGTH: 1356
; TYPE: PRT
; ORGANISM: Corononavirus-HKU1
US-11-129-741-2949

Query Match 86.0%; Score 37; DB 6; Length 1356;
Best Local Similarity 77.8%; Pred. No. 1.9e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RSVSLSYRF 9
||:|||||
Db 760 RSISASYRF 768

RESULT 8

US-11-129-741-2951
; Sequence 2951, Application US/11129741
; Publication No. US20060034853A1
; GENERAL INFORMATION:
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: WOO, CHIU YAT PATRICK
; APPLICANT: LAU, KAR PUI SUSANNA
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: POON, LIT MAN
; APPLICANT: PEIRIS, JOSEPH S.M.
; APPLICANT: GUAN, YI
; TITLE OF INVENTION: A NOVEL HUMAN VIRUS CAUSING RESPIRATORY TRACT
; FILE REFERENCE: V0690.0044
; CURRENT APPLICATION NUMBER: US/11/129,741
; CURRENT FILING DATE: 2005-05-16

; PRIOR APPLICATION NUMBER: 10/895,064
; PRIOR FILING DATE: 2004-07-21
; NUMBER OF SEQ ID NOS: 4257
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2951
; LENGTH: 1356
; TYPE: PRT
; ORGANISM: Corononavirus-HKU1
US-11-129-741-2951

Query Match 86.0%; Score 37; DB 6; Length 1356;
Best Local Similarity 77.8%; Pred. No. 1.9e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RSVSLSYRF 9
||:|||||
Db 760 RSISASYRF 768

RESULT 9

US-11-129-741-4245
; Sequence 4245, Application US/11129741
; Publication No. US20060034853A1
; GENERAL INFORMATION:
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: WOO, CHIU YAT PATRICK
; APPLICANT: LAU, KAR PUI SUSANNA
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: POON, LIT MAN
; APPLICANT: PEIRIS, JOSEPH S.M.
; APPLICANT: GUAN, YI
; TITLE OF INVENTION: A NOVEL HUMAN VIRUS CAUSING RESPIRATORY TRACT
; FILE REFERENCE: V0690.0044
; CURRENT APPLICATION NUMBER: US/11/129,741
; PRIOR FILING DATE: 2005-05-16
; PRIOR APPLICATION NUMBER: 10/895,064
; PRIOR FILING DATE: 2004-07-21
; NUMBER OF SEQ ID NOS: 4257
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4245
; LENGTH: 1356
; TYPE: PRT
; ORGANISM: Corononavirus-HKU1
US-11-129-741-4245

Query Match 86.0%; Score 37; DB 6; Length 1356;
Best Local Similarity 77.8%; Pred. No. 1.9e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RSVSLSYRF 9
||:|||||
Db 760 RSISASYRF 768

RESULT 10

US-10-895-064-420
; Sequence 420, Application US/10895064
; Publication No. US20060018923A1
; GENERAL INFORMATION:
; APPLICANT: PEIRIS, JOSEPH S.M.
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: POON, LIT MAN
; APPLICANT: GUAN, YI
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: NICHOLLS, JOHN M.
; APPLICANT: LEUNG, FREDERICK C.
; TITLE OF INVENTION: A NOVEL HUMAN VIRUS CAUSING RESPIRATORY TRACT INFECTION AND USES
; FILE REFERENCE: V0690.0031
; CURRENT APPLICATION NUMBER: US/10/895,064
; CURRENT FILING DATE: 2004-07-21
; NUMBER OF SEQ ID NOS: 2918

```
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 420
; LENGTH: 1362
; TYPE: PRT
; ORGANISM: Corononavirus-HKU1
US-10-895-064-420

Query Match      86.0%; Score 37; DB 5; Length 1362;
Best Local Similarity 77.8%; Pred. No. 1.9e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RSVLSYRF 9
Db 766 RSISASYRF 774

RESULT 11
US-11-129-741-420
; Sequence 420, Application US/11129741
; Publication No. US20060034853A1
; GENERAL INFORMATION:
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: WOO, CHIU YAT PATRICK
; APPLICANT: LAU, KAR PUI SUSANNA
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: POON, LIT MAN
; APPLICANT: PEIRIS, JOSEPH S.M.
; APPLICANT: GUAN, YI
; TITLE OF INVENTION: A NOVEL HUMAN VIRUS CAUSING RESPIRATORY TRACT
; TITLE OF INVENTION: INFECTION AND USES THEREOF
; FILE REFERENCE: V0690.0044
; CURRENT APPLICATION NUMBER: US/11/129,741
; CURRENT FILING DATE: 2005-05-16
; PRIOR APPLICATION NUMBER: 10/895,064
; PRIOR FILING DATE: 2004-07-21
; NUMBER OF SEQ ID NOS: 4257
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 420
; LENGTH: 1362
; TYPE: PRT
; ORGANISM: Corononavirus-HKU1
US-11-129-741-420

Query Match      86.0%; Score 37; DB 6; Length 1362;
Best Local Similarity 77.8%; Pred. No. 1.9e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RSVLSYRF 9
Db 766 RSISASYRF 774

RESULT 12
US-10-222-703A-831
; Sequence 831, Application US/10222703A
; Publication No. US20050059584A1
; GENERAL INFORMATION:
; APPLICANT: MERZOUK, AHMED
; APPLICANT: HABI, ABDELKRIM
; APPLICANT: WONG, DONALD
; APPLICANT: SALARI, HASSAN
; TITLE OF INVENTION: NOVEL CHEMOKINE MIMETICS SYNTHESIS AND THEIR USE
; FILE REFERENCE: 592960-00002
; CURRENT APPLICATION NUMBER: US/10/222,703A
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: 10/086,177
; PRIOR FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: 09/835,107
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/373,629
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/373,628
; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 868
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 831
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: (2)..(2)
; OTHER INFORMATION: D-Pro
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (5)..(5)
; OTHER INFORMATION: D-Leu
US-10-222-703A-833

Query Match      81.4%; Score 35; DB 5; Length 14;
Best Local Similarity 77.8%; Pred. No. 3.9;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RSVLSYRF 9
Db 1 KPVLSYRF 9

RESULT 13
US-10-222-703A-833
; Sequence 833, Application US/10222703A
; Publication No. US20050059584A1
; GENERAL INFORMATION:
; APPLICANT: MERZOUK, AHMED
; APPLICANT: HABI, ABDELKRIM
; APPLICANT: WONG, DONALD
; APPLICANT: SALARI, HASSAN
; TITLE OF INVENTION: NOVEL CHEMOKINE MIMETICS SYNTHESIS AND THEIR USE
; FILE REFERENCE: 592960-00002
; CURRENT APPLICATION NUMBER: US/10/222,703A
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: 10/086,177
; PRIOR FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: 09/835,107
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/373,629
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/373,628
; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 868
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 833
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: (2)..(2)
; OTHER INFORMATION: D-Pro
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (5)..(5)
; OTHER INFORMATION: D-Leu
US-10-222-703A-833

Query Match      81.4%; Score 35; DB 5; Length 14;
Best Local Similarity 77.8%; Pred. No. 3.9;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RSVLSYRF 9
Db 1 KPVLSYRF 9

RESULT 14
US-10-222-703A-855
; Sequence 855, Application US/10222703A
; Publication No. US20050059584A1
; GENERAL INFORMATION:
; APPLICANT: MERZOUK, AHMED
```


; APPLICANT: HABI, ABDELKRIM
; APPLICANT: WONG, DONALD
; APPLICANT: SALARI, HASSAN
; TITLE OF INVENTION: NOVEL CHEMOKINE MIMETICS SYNTHESIS AND THEIR USE
; FILE REFERENCE: 592960-00002
; CURRENT APPLICATION NUMBER: US/10/222,703A
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: 10/086,177
; PRIOR FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: 09/835,107
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/373,629
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/373,628
; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 868
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 855
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-222-703A-855

Query Match 81.4%; Score 35; DB 5; Length 14;
Best Local Similarity 77.8%; Pred. No. 3.9;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RSVLSLYRF 9
: |||||
Db 1 KPVLSLYRF 9

RESULT 15
US-10-222-703A-857
; Sequence 857, Application US/10222703A
; Publication No. US20050059584A1
; GENERAL INFORMATION:
; APPLICANT: MERZOUK, AHMED
; APPLICANT: HABI, ABDELKRIM
; APPLICANT: WONG, DONALD
; APPLICANT: SALARI, HASSAN
; TITLE OF INVENTION: NOVEL CHEMOKINE MIMETICS SYNTHESIS AND THEIR USE
; FILE REFERENCE: 592960-00002
; CURRENT APPLICATION NUMBER: US/10/222,703A
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: 10/086,177
; PRIOR FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: 09/835,107
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/373,629
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/373,628
; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 868
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 857
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (2)-(2)
; OTHER INFORMATION: D-Pro
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (5)-(5)
; OTHER INFORMATION: D-Leu
US-10-222-703A-857

Query Match 81.4%; Score 35; DB 5; Length 14;
Best Local Similarity 77.8%; Pred. No. 3.9;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RSVLSLYRF 9
: |||||
Db 1 KPVLSLYRF 9

Search completed: August 10, 2006, 23:19:37
Job time : 103.636 secs

THIS PAGE BLANK (USPTO)

Result No.	Score	Query Match	Length	DB	ID	Description	
1	43	100.0	9	8	ADU18130	Adul18130	Immune ce
2	43	100.0	9	8	ADU18134	Adul18134	Immune ce
3	37	86.0	1362	10	AEF31834	Aef31834	Human con
4	35	81.4	13	2	AAY08435	Aay08435	CXCR-4 re
5	35	81.4	27	9	ADY76935	Ady76935	Chemokine
6	35	81.4	27	9	ADY77047	Ady77047	Chemokine
7	35	81.4	27	9	ADY77011	Ady77011	Chemokine
8	35	81.4	27	9	ADY76971	Ady76971	Chemokine
9	35	81.4	31	9	ADY77010	Ady77010	Chemokine
10	35	81.4	31	9	ADY77046	Ady77046	Chemokine
11	35	81.4	31	9	ADY76934	Ady76934	Chemokine
12	35	81.4	31	9	ADY76970	Ady76970	Chemokine
13	34	79.1	26	9	ADY76973	Ady76973	Chemokine
14	34	79.1	26	9	ADY77013	Ady77013	Chemokine
15	34	79.1	26	9	ADY77049	Ady77049	Chemokine
16	34	79.1	26	9	ADY76937	Ady76937	Chemokine
17	34	79.1	30	9	ADY77012	Ady77012	Chemokine
18	34	79.1	30	9	ADY77048	Ady77048	Chemokine
19	34	79.1	30	9	ADY76972	Ady76972	Chemokine
20	34	79.1	30	9	ADY76936	Ady76936	Chemokine
21	34	79.1	559	3	AAY19171	Aay19171	PMWav-2 R
22	33	76.7	9	8	ADU18131	Adul18131	Immune ce
23	32	74.4	13	2	AAY08436	Aay08436	CXCR-4 re

CC The invention relates to an isolated peptide having an amino terminus and
 CC a carboxy terminus, selected from four amino acid sequences (A1), (A2),
 CC (A3) and (A4), respectively, (A1: ADU18132), (A2: ADU18131), (A3:
 CC ADU18134) and H2N-Arg-Ser(-O-R1)-Val-Ser-Leu-Ser-Tyr-Arg(-H2N-Phe-O-CH2(-
 CC CH(-CH2-O-R3)-O-R2))-Phe-O-CH2(-CH(-CH2-O-R3)-O-R2) (A4: ADU18130),
 CC respectively where R1-R3 are fatty acid groups (preferably stearic acid,
 CC arachidic acid or arachidonic acid). The peptides can be used for the
 CC treatment or prevention of a mammalian disease or disorder such as,
 CC bacterial, viral or parasitic infections and/or cancer or neoplasia, such
 CC as cholera, dysentery, influenza and tuberculosis, as a prophylactic for
 CC short term protection in a bioterrorism area and other contagion environs
 CC and in patients undergoing major surgery to prevent post-operative
 CC infections, as a vaccine adjuvant to provide long-term protection, and
 CC also useful in adjunctive therapy. The peptides act as immune cell
 CC potentiating factors (ICPF) i.e. immune regulators, exhibit a broad
 CC spectrum of therapeutic efficiency and a wide margin of safety to the
 CC host species with respect to toxic and fetal side effects, as associated
 CC with the prior art ICPFs. The peptides are effective in an amount that
 CC produces a serum concentration of greater than 1 microgram/ml, and are
 CC capable of providing an affordable therapy for serious infectious
 CC diseases. This sequence corresponds to a peptide of the invention
 CC isolated from goat serum.

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 43; DB 8; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSVSLSYRF 9
 |||||
 Db 1 RSVSLSYRF 9

RESULT 2

ADU18134
 ID ADU18134 standard; peptide; 9 AA.

AC ADU18134;

XX 27-JAN-2005 (first entry)

XX Immune cell potentiating factor peptide #5.

XX immunostimulant; cytostatic; antimicrobial; antibacterial; virucide;
 KW antiparasitic; antitubercular; tuberculostatic; immune modulation;
 KW bacterial infection; viral infection; parasitic infection; cancer;
 KW neoplasia; bioterrorism; surgery; post-operative infection;
 KW vaccine adjuvant; immune cell potentiating factor.

XX Capra hircus.

OS Synthetic.

XX WO2004094455-A2.

XX 04-NOV-2004.

XX 16-APR-2004; 2004WO-US011896.

XX 16-APR-2003; 2003US-0463042P.

XX (GENE-) GENEBACT BIOTECHNOLOGIES INC.

XX Thacker JD, Fuhrer PJ, Willeford KO;

XX WPI; 2004-795526/78.

XX New isolated peptides having an amino terminus and a carboxy terminus
 PT useful for the treatment or prevention of viral and bacterial infections,
 PT comprise amino acids as given in the specification.

XX Claim 12; SEQ ID NO 5; 55pp; English.

CC The invention relates to an isolated peptide having an amino terminus and
 CC a carboxy terminus, selected from four amino acid sequences (A1), (A2),
 CC (A3) and (A4), respectively, (A1: ADU18132), (A2: ADU18131), (A3:
 CC ADU18134) and H2N-Arg-Ser(-O-R1)-Val-Ser-Leu-Ser-Tyr-Arg(-H2N-Phe-O-CH2(-
 CC CH(-CH2-O-R3)-O-R2))-Phe-O-CH2(-CH(-CH2-O-R3)-O-R2) (A4: ADU18130),
 CC respectively where R1-R3 are fatty acid groups (preferably stearic acid,
 CC arachidic acid or arachidonic acid). The peptides can be used for the
 CC treatment or prevention of a mammalian disease or disorder such as,
 CC bacterial, viral or parasitic infections and/or cancer or neoplasia, such
 CC as cholera, dysentery, influenza and tuberculosis, as a prophylactic for
 CC short term protection in a bioterrorism area and other contagion environs
 CC and in patients undergoing major surgery to prevent post-operative
 CC infections, as a vaccine adjuvant to provide long-term protection, and
 CC also useful in adjunctive therapy. The peptides act as immune cell
 CC potentiating factors (ICPF) i.e. immune regulators, exhibit a broad
 CC spectrum of therapeutic efficiency and a wide margin of safety to the
 CC host species with respect to toxic and fetal side effects, as associated
 CC with the prior art ICPFs. The peptides are effective in an amount that
 CC produces a serum concentration of greater than 1 microgram/ml, and are
 CC capable of providing an affordable therapy for serious infectious
 CC diseases. This sequence corresponds to a peptide of the invention.

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 43; DB 8; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSVSLSYRF 9
 |||||
 Db 1 RSVSLSYRF 9

RESULT 3

AEF31834
 ID AEF31834 standard; protein; 1362 AA.

AC AEF31834;

XX 23-MAR-2006 (first entry)

XX Human coronavirus HKU1 amino acid sequence SEQ ID NO:420.

XX virucide; respiratory-gen.; vaccine; respiratory tract infection.

XX Human coronavirus HKU1.

XX US2006018923-A1.

XX 26-JAN-2006.

XX 21-JUL-2004; 2004US-00895064.

XX 21-JUL-2004; 2004US-00895064.

XX (YUEN/) YUEN K Y.

XX (WOOC/) WOO C Y P.

XX (LAUK/) LAU K P S.

XX (CHAN/) CHAN K H.

XX (POON/) POON L M.

XX (PEIR/) PEIRIS J S M.

XX (GUAN/) GUAN Y.

XX Yuen KY, Woo CYP, Lau KPS, Chan KH, Poon LM, Peiris JSM, Guan Y;

XX WPI; 2006-109168/11.

XX New nucleic acid molecule encoding human virus, useful for preventing,
 PT diagnosing, and/or treating infection caused by coronavirus-HKU1, e.g.
 PT respiratory tract infection.

XX Claim 20; SEQ ID NO 420; 141pp; English.

CC The invention relates to an isolated nucleic acid molecule comprising the
 CC nucleotide sequence of AEF31415 or AEF31417, or its complement, or a
 CC nucleotide sequence encoding the amino acid sequence of AEF31416 or a
 CC complement of the nucleotide sequence. Also described: (1) a vector
 CC comprising the nucleic acid molecule above; (2) a host cell comprising
 CC the vector of (1) or the nucleic acid molecule above operably linked to a
 CC heterologous promoter; (3) producing a polypeptide; (4) preparing a cell
 CC or its progeny, capable of expressing a polypeptide; (5) an isolated
 CC polypeptide encoded by the nucleic acid molecule above; (6) an isolated
 CC antibody or its antigen-binding fragment, which immunospecifically binds
 CC to the polypeptide of (5); (7) detecting the presence of the polypeptide
 CC of (5) in a biological sample; (8) detecting the presence of a first
 CC nucleic acid molecule comprising the nucleotide sequence of AEF31415 or
 CC AEF31417, or its fragment or complement, in a biological sample; (9)
 CC preventing or inhibiting a replication in a host cell of a nucleic acid
 CC molecule comprising the nucleotide sequence of AEF31415 and/or AEF31417,
 CC or its portion or complement; (10) preventing or inhibiting a binding to
 CC a host cell of the polypeptide encoded by a nucleotide sequence of
 CC AEF31415 or AEF31417, or its fragment or complement; (11) detecting the
 CC presence of an antibody in a biological sample that immunospecifically
 CC binds the polypeptides of (5); (12) identifying a subject infected with
 CC human coronavirus HKU1 (CoV-HKU1); and (13) an immunogenic formulation
 CC comprising an immunogenic amount of the polypeptide of (5), or the
 CC nucleic acid molecule comprising the nucleotide sequence of AEF31415 or
 CC AEF31417, its complement or fragment, and a pharmaceutical carrier. The
 CC CoV-HKU1 sequences, composition, vaccine, and method of the invention are
 CC useful for preventing, diagnosing, and/or treating infection caused by
 CC CoV-HKU1, e.g. respiratory tract infection. The present sequence
 CC represents a first frame translation amino acid sequence from the CoV-
 CC HKU1 entire genomic DNA sequence of AEF31417, which is used in the
 CC exemplification of the present invention. Note - The sequence listing for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from the USPTO web site. However
 CC all the sequences do appear in either the figures or the disclosure of
 CC the specification.

XX
 SQ Sequence 1362 AA;

Query Match 86.0%; Score 37; DB 10; Length 1362;
 Best Local Similarity 77.8%; Pred. No. 2.1e+02;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RSVSLSYRF 9
 ||:| ||||
 Db 766 RSISASYRF 774

RESULT 4
 AAY08435
 ID AAY08435 standard; peptide; 13 AA.

AC AAY08435;

DT 26-JUL-1999 (first entry)

DE CXCR-4 receptor binding peptide 20.

XX CXCR-4 receptor; antagonist; stroma cell-derived factor-1; SDF-1; HIV-1;
 KW infection; lymphotropic strain; treatment; diagnosis.

OS Synthetic.

XX DE19734161-A1.

XX 01-APR-1999.

XX 07-AUG-1997; 97DE-01034161.

XX 07-AUG-1997; 97DE-01034161.

XX (JERI-) JERINI BIOTOOLS GMBH.

PI Schneider-Mergener J, Germeroth L, Heveker N, Allison M;

XX

DR WPI; 1999-230182/20.

XX

PT Antagonists of stroma cell-derived factor-1, for diagnosis and treatment
 of human immune deficiency virus (HIV) infection.

XX

PS Disclosure; Page 17; 20pp; German.

XX

CC This invention describes novel antagonists of stroma cell-derived factor-
 1 (SDF-1) which bind to the CXCR-4 receptor, to which SDF-1 normally
 CC binds, so prevents binding of this receptor to HIV-1, an essential step
 CC in infection by lymphotropic strains of the virus. The peptides of the
 CC invention (AAY08416-Y08438) are used to treat or diagnose human immune
 CC deficiency virus-1 (HIV-1) infection and provide, for the first time, a
 CC method for antagonizing the interaction between HIV-1 and the CXCR-4
 CC receptor

SQ Sequence 13 AA;

Query Match 81.4%; Score 35; DB 2; Length 13;
 Best Local Similarity 77.8%; Pred. No. 3.4;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RSVSLSYRF 9
 : |||||
 Db 1 KPVSLSYRF 9

RESULT 5

ADY76935
 ID ADY76935 standard; peptide; 27 AA.

XX AC ADY76935;

XX 02-JUN-2005 (first entry)

DE Chemokine analog peptide #24.

XX chemokine; inflammation; antiinflammatory; autoimmune disease;
 KW immunosuppressive; cancer; cytostatic; cardiovascular disease;
 KW cardiovascular-gen.; infection; rheumatoid arthritis; antiarthritic;
 KW antirheumatic; chronic inflammatory bowel disease; antiinflammatory;
 KW gastrointestinal-gen.; multiple sclerosis; neuroprotective; asthma;
 KW antiasthmatic; osteoarthritis; osteopathic; atherosclerosis;
 KW antiarteriosclerotic; psoriasis; antipsoriatic; rhinitis; antiallergic;
 KW organ transplant rejection.

XX Synthetic.

OS Unidentified.

XX US2005059584-A1.

XX 17-MAR-2005.

XX 16-AUG-2002; 2002US-00222703.

XX 16-AUG-2002; 2002US-00222703.

XX (MERZ/) MERZOUK A.

XX (HABI/) HABI A.

XX (WONG/) WONG D.

XX (SALA/) SALARI H.

XX Merzouk A, Habi A, Wong D, Salari H;

XX WPI; 2005-232172/24.

XX Chemokine derived analog compound, useful for treating autoimmune
 PT diseases, chronic inflammation, cancer, cardiovascular disease, or
 PT infectious disease.

XX Example 17; Fig 17; 104pp; English.

XX

CC The invention comprises chemokine derived analog peptides, such as
 CC stromal cell-derived factor-1 (SDF-1) peptides or macrophage inflammatory
 CC protein-1-alpha (MIP-1-alpha) peptides. The chemokine derived analog
 CC peptides of the invention are useful for treating inflammation,
 CC autoimmune diseases, cancer, cardiovascular disease, infections,
 CC rheumatoid arthritis, chronic inflammatory bowel disease, chronic
 CC inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis,
 CC atherosclerosis, psoriasis, rhinitis, and organ transplant rejection. The
 CC present amino acid sequence represents a chemokine analog peptide that
 CC was used in an example of the invention.

XX Sequence 27 AA;

Query Match 81.4%; Score 35; DB 9; Length 27;
 Best Local Similarity 77.8%; Pred. No. 7.4;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RSVLSLYRF 9
 : |||||
 Db 1 KPVLSLYRF 9

RESULT 6
 ADY77047
 ID ADY77047 standard; peptide; 27 AA.

XX AC ADY77047;

XX DT 02-JUN-2005 (first entry)

XX DE Chemokine analog peptide #136.

XX chemokine; inflammation; antiinflammatory; autoimmune disease;
 KW immunosuppressive; cancer; cytostatic; cardiovascular disease;
 KW cardiovascular-gen.; infection; rheumatoid arthritis; antiarthritic;
 KW antirheumatic; chronic inflammatory bowel disease; antiinflammatory;
 KW gastrointestinal-gen.; multiple sclerosis; neuroprotective; asthma;
 KW antiasthmatic; osteoarthritis; osteopathic; atherosclerosis;
 KW antiarteriosclerotic; psoriasis; osteopathic; atherosclerosis;
 KW organ transplant rejection.

XX Synthetic.
 OS Unidentified.

XX PN US2005059584-A1.

XX PD 17-MAR-2005.

XX PF 16-AUG-2002; 2002US-00222703.

XX PR 16-AUG-2002; 2002US-00222703.

XX PA (MERZ/) MERZOUK A.
 PA (HABI/) HABI A.
 PA (WONG/) WONG D.
 PA (SALA/) SALARI H.

PI Merzouk A, Habi A, Wong D, Salari H;

XX WPI; 2005-232172/24.

XX Chemokine derived analog compound, useful for treating autoimmune
 PT diseases, chronic inflammation, cancer, cardiovascular disease, or
 PT infectious disease.

XX Example 17; Fig 17; 104pp; English.

XX The invention comprises chemokine derived analog peptides, such as
 CC stromal cell-derived factor-1 (SDF-1) peptides or macrophage inflammatory
 CC protein-1-alpha (MIP-1-alpha) peptides. The chemokine derived analog
 CC peptides of the invention are useful for treating inflammation,
 CC autoimmune diseases, cancer, cardiovascular disease, infections,
 CC rheumatoid arthritis, chronic inflammatory bowel disease, chronic

CC inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis,
 CC atherosclerosis, psoriasis, rhinitis, and organ transplant rejection. The
 CC present amino acid sequence represents a chemokine analog peptide that
 CC was used in an example of the invention.

XX Sequence 27 AA;

Query Match 81.4%; Score 35; DB 9; Length 27;
 Best Local Similarity 77.8%; Pred. No. 7.4;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RSVLSLYRF 9
 : |||||
 Db 1 KPVLSLYRF 9

RESULT 7
 ADY77011
 ID ADY77011 standard; peptide; 27 AA.

XX AC ADY77011;

XX DT 02-JUN-2005 (first entry)

XX DE Chemokine analog peptide #100.

XX chemokine; inflammation; antiinflammatory; autoimmune disease;
 KW immunosuppressive; cancer; cytostatic; cardiovascular disease;
 KW cardiovascular-gen.; infection; rheumatoid arthritis; antiarthritic;
 KW antirheumatic; chronic inflammatory bowel disease; antiinflammatory;
 KW gastrointestinal-gen.; multiple sclerosis; neuroprotective; asthma;
 KW antiasthmatic; osteoarthritis; osteopathic; atherosclerosis;
 KW antiarteriosclerotic; psoriasis; osteopathic; atherosclerosis;
 KW organ transplant rejection.

XX Synthetic.
 OS Unidentified.

XX PN US2005059584-A1.

XX PD 17-MAR-2005.

XX PF 16-AUG-2002; 2002US-00222703.

XX PR 16-AUG-2002; 2002US-00222703.

XX PA (MERZ/) MERZOUK A.
 PA (HABI/) HABI A.
 PA (WONG/) WONG D.
 PA (SALA/) SALARI H.

PI Merzouk A, Habi A, Wong D, Salari H;

XX WPI; 2005-232172/24.

XX Chemokine derived analog compound, useful for treating autoimmune
 PT diseases, chronic inflammation, cancer, cardiovascular disease, or
 PT infectious disease.

XX Example 17; Fig 17; 104pp; English.

XX The invention comprises chemokine derived analog peptides, such as
 CC stromal cell-derived factor-1 (SDF-1) peptides or macrophage inflammatory
 CC protein-1-alpha (MIP-1-alpha) peptides. The chemokine derived analog
 CC peptides of the invention are useful for treating inflammation,
 CC autoimmune diseases, cancer, cardiovascular disease, infections,
 CC rheumatoid arthritis, chronic inflammatory bowel disease, chronic
 CC inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis,
 CC atherosclerosis, psoriasis, rhinitis, and organ transplant rejection. The
 CC present amino acid sequence represents a chemokine analog peptide that
 CC was used in an example of the invention.

XX Sequence 27 AA;

Query Match 81.4%; Score 35; DB 9; Length 27;
 Best Local Similarity 77.8%; Pred. NO. 7.4;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RSVLSYRF 9
 : |||||
 Db 1 KPVSLSYRF 9

RESULT 8
 ADY76971
 ID ADY76971 standard; peptide; 27 AA.
 XX
 AC ADY76971;
 DT 02-JUN-2005 (first entry)
 DE Chemokine analog peptide #60.
 XX chemokine; inflammation; antiinflammatory; autoimmune disease;
 KW immunosuppressive; cancer; cytostatic; cardiovascular disease;
 KW cardiovascular-gen.; infection; rheumatoid arthritis; antiarthritic;
 KW antirheumatic; chronic inflammatory bowel disease; antiinflammatory;
 KW gastrointestinal-gen.; multiple sclerosis; neuroprotective; asthma;
 KW antiasthmatic; osteoarthritis; osteopathic; atherosclerosis;
 KW antiarteriosclerotic; psoriasis; antipsoriatic; rhinitis; antiallergic;
 KW organ transplant rejection.
 XX Synthetic.
 OS Unidentified.
 XX US2005059584-A1.
 PN 17-MAR-2005.
 PD 16-AUG-2002; 2002US-00222703.
 PF 16-AUG-2002; 2002US-00222703.
 XX 16-AUG-2002; 2002US-00222703.
 PR (MERZ/) MERZOUK A.
 PA (HABI/) HABI A.
 PA (WONG/) WONG D.
 PA (SALA/) SALARI H.
 XX Merzouk A, Habi A, Wong D, Salari H;
 PI WPI; 2005-232172/24.
 DR Chemokine derived analog compound, useful for treating autoimmune
 PT diseases, chronic inflammation, cancer, cardiovascular disease, or
 PT infectious disease.
 XX Example 17; Fig 17; 104pp; English.
 PS The invention comprises chemokine derived analog peptides, such as
 CC stromal cell-derived factor-1 (SDF-1) peptides or macrophage inflammatory
 CC protein-1-alpha (MIP-1-alpha) peptides. The chemokine derived analog
 CC peptides of the invention are useful for treating inflammation,
 CC autoimmune diseases, cancer, cardiovascular disease, infections,
 CC rheumatoid arthritis, chronic inflammatory bowel disease, chronic
 CC inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis,
 CC atherosclerosis, psoriasis, rhinitis, and organ transplant rejection. The
 CC present amino acid sequence represents a chemokine analog peptide that
 CC was used in an example of the invention.
 XX Sequence 27 AA;
 SQ

Query Match 81.4%; Score 35; DB 9; Length 27;
 Best Local Similarity 77.8%; Pred. NO. 7.4;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RSVLSYRF 9
 : |||||
 Db 1 KPVSLSYRF 9

RESULT 9
 ADY77010
 ID ADY77010 standard; peptide; 31 AA.
 XX
 AC ADY77010;
 DT 02-JUN-2005 (first entry)
 DE Chemokine analog peptide #99.
 XX chemokine; inflammation; antiinflammatory; autoimmune disease;
 KW immunosuppressive; cancer; cytostatic; cardiovascular disease;
 KW cardiovascular-gen.; infection; rheumatoid arthritis; antiarthritic;
 KW antirheumatic; chronic inflammatory bowel disease; antiinflammatory;
 KW gastrointestinal-gen.; multiple sclerosis; neuroprotective; asthma;
 KW antiasthmatic; osteoarthritis; osteopathic; atherosclerosis;
 KW antiarteriosclerotic; psoriasis; antipsoriatic; rhinitis; antiallergic;
 KW organ transplant rejection.
 XX Synthetic.
 OS Unidentified.
 XX US2005059584-A1.
 PN 17-MAR-2005.
 PD 16-AUG-2002; 2002US-00222703.
 PF 16-AUG-2002; 2002US-00222703.
 XX 16-AUG-2002; 2002US-00222703.
 PR (MERZ/) MERZOUK A.
 PA (HABI/) HABI A.
 PA (WONG/) WONG D.
 PA (SALA/) SALARI H.
 XX Merzouk A, Habi A, Wong D, Salari H;
 PI WPI; 2005-232172/24.
 DR Chemokine derived analog compound, useful for treating autoimmune
 PT diseases, chronic inflammation, cancer, cardiovascular disease, or
 PT infectious disease.
 XX Example 17; Fig 17; 104pp; English.
 PS The invention comprises chemokine derived analog peptides, such as
 CC stromal cell-derived factor-1 (SDF-1) peptides or macrophage inflammatory
 CC protein-1-alpha (MIP-1-alpha) peptides. The chemokine derived analog
 CC peptides of the invention are useful for treating inflammation,
 CC autoimmune diseases, cancer, cardiovascular disease, infections,
 CC rheumatoid arthritis, chronic inflammatory bowel disease, chronic
 CC inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis,
 CC atherosclerosis, psoriasis, rhinitis, and organ transplant rejection. The
 CC present amino acid sequence represents a chemokine analog peptide that
 CC was used in an example of the invention.
 XX Sequence 31 AA;
 SQ

Query Match 81.4%; Score 35; DB 9; Length 31;
 Best Local Similarity 77.8%; Pred. NO. 8.7;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RSVLSYRF 9
 : |||||
 Db 1 KPVSLSYRF 9

RESULT 10
 ADY77046

```

ID ADY77046 standard; peptide; 31 AA.
XX
AC ADY77046;
XX
DT 02-JUN-2005 (first entry)
XX
DE Chemokine analog peptide #135.
XX
KW chemokine; inflammation; antiinflammatory; autoimmune disease;
KW immunosuppressive; cancer; cytostatic; cardiovascular disease;
KW cardiovascular-gen.; infection; rheumatoid arthritis; antiarthritic;
KW antirheumatic; chronic inflammatory bowel disease; antiinflammatory;
KW gastrointestinal-gen.; multiple sclerosis; neuroprotective; asthma;
KW antiasthmatic; osteoarthritis; osteopathic; atherosclerosis;
KW antiarteriosclerotic; psoriasis; antipsoriatic; rhinitis; antiallergic;
KW organ transplant rejection.
XX
OS Synthetic.
OS Unidentified.
XX
PN US2005059584-A1.
XX
PD 17-MAR-2005.
XX
PF 16-AUG-2002; 2002US-00222703.
XX
PR 16-AUG-2002; 2002US-00222703.
XX
PA (MERZ/) MERZOUK A.
PA (HABI/) HABI A.
PA (WONG/) WONG D.
PA (SALA/) SALARI H.
XX
PI Merzouk A, Habi A, Wong D, Salari H;
XX
DR WPI; 2005-232172/24.
XX
PT Chemokine derived analog compound, useful for treating autoimmune
PT diseases, chronic inflammation, cancer, cardiovascular disease, or
PT infectious disease.
XX
PS Example 17; Fig 17; 104pp; English.
XX
The invention comprises chemokine derived analog peptides, such as
CC stromal cell-derived factor-1 (SDF-1) peptides or macrophage inflammatory
CC protein-1-alpha (MIP-1-alpha) peptides. The chemokine derived analog
CC peptides of the invention are useful for treating inflammation,
CC autoimmune diseases, cancer, cardiovascular disease, infections,
CC rheumatoid arthritis, chronic inflammatory bowel disease, chronic
CC inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis,
CC atherosclerosis, psoriasis, rhinitis, and organ transplant rejection. The
CC present amino acid sequence represents a chemokine analog peptide that
CC was used in an example of the invention.
XX
SQ Sequence 31 AA;
Query Match 81.4%; Score 35; DB 9; Length 31;
Best Local Similarity 77.8%; Pred. No. 8.7;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Oy 1 RSVSLSYRF 9
Db 1 KPVSLSYRF 9
: |||||
RESULT 11
ADY76934
ID ADY76934 standard; peptide; 31 AA.
XX
AC ADY76934;
XX
DT 02-JUN-2005 (first entry)
XX
DE Chemokine analog peptide #135.
XX
KW chemokine; inflammation; antiinflammatory; autoimmune disease;
KW immunosuppressive; cancer; cytostatic; cardiovascular disease;
KW cardiovascular-gen.; infection; rheumatoid arthritis; antiarthritic;
KW antirheumatic; chronic inflammatory bowel disease; antiinflammatory;
KW gastrointestinal-gen.; multiple sclerosis; neuroprotective; asthma;
KW antiasthmatic; osteoarthritis; osteopathic; atherosclerosis;
KW antiarteriosclerotic; psoriasis; antipsoriatic; rhinitis; antiallergic;
KW organ transplant rejection.
XX
OS Synthetic.
OS Unidentified.
XX
PN US2005059584-A1.
XX
PD 17-MAR-2005.
XX
PF 16-AUG-2002; 2002US-00222703.
XX
PR 16-AUG-2002; 2002US-00222703.
XX
PA (MERZ/) MERZOUK A.
PA (HABI/) HABI A.
PA (WONG/) WONG D.
PA (SALA/) SALARI H.
XX
PI Merzouk A, Habi A, Wong D, Salari H;
XX
DR WPI; 2005-232172/24.
XX
PT Chemokine derived analog compound, useful for treating autoimmune
PT diseases, chronic inflammation, cancer, cardiovascular disease, or
PT infectious disease.
XX
PS Example 17; Fig 17; 104pp; English.
XX
The invention comprises chemokine derived analog peptides, such as
CC stromal cell-derived factor-1 (SDF-1) peptides or macrophage inflammatory
CC protein-1-alpha (MIP-1-alpha) peptides. The chemokine derived analog
CC peptides of the invention are useful for treating inflammation,
CC autoimmune diseases, cancer, cardiovascular disease, infections,
CC rheumatoid arthritis, chronic inflammatory bowel disease, chronic
CC inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis,
CC atherosclerosis, psoriasis, rhinitis, and organ transplant rejection. The
CC present amino acid sequence represents a chemokine analog peptide that
CC was used in an example of the invention.
XX
SQ Sequence 31 AA;
Query Match 81.4%; Score 35; DB 9; Length 31;
Best Local Similarity 77.8%; Pred. No. 8.7;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Oy 1 RSVSLSYRF 9
Db 1 KPVSLSYRF 9
: |||||
RESULT 12
ADY76970
ID ADY76970 standard; peptide; 31 AA.
XX
AC ADY76970;
XX
DT 02-JUN-2005 (first entry)
XX
DE Chemokine analog peptide #59.
XX
KW chemokine; inflammation; antiinflammatory; autoimmune disease;
KW immunosuppressive; cancer; cytostatic; cardiovascular disease;
KW cardiovascular-gen.; infection; rheumatoid arthritis; antiarthritic;
KW antirheumatic; chronic inflammatory bowel disease; antiinflammatory;

```


KW gastrointestinal-gen.; multiple sclerosis; neuroprotective; asthma;
 KW antiasthmatic; osteoarthritis; osteopathic; atherosclerosis;
 KW antiarteriosclerotic; psoriasis; antipsoriatic; rhinitis; antiallergic;
 KW organ transplant rejection.

XX Synthetic.
 OS Unidentified.

XX US2005059584-A1.
 PN 17-MAR-2005.

XX 16-AUG-2002; 2002US-00222703.

XX 16-AUG-2002; 2002US-00222703.

XX (MERZ/) MERZOUK A.
 PA (HABI/) HABI A.
 PA (WONG/) WONG D.
 PA (SALA/) SALARI H.

XX Merzouk A, Habi A, Wong D, Salari H;
 PI WPI; 2005-232172/24.

XX Chemokine derived analog compound, useful for treating autoimmune
 PT diseases, chronic inflammation, cancer, cardiovascular disease, or
 PT infectious disease.

XX Example 17; Fig 17; 104pp; English.

PS The invention comprises chemokine derived analog peptides, such as
 CC stromal cell-derived factor-1 (SDF-1) peptides or macrophage inflammatory
 CC protein-1-alpha (MIP-1-alpha) peptides. The chemokine derived analog
 CC peptides of the invention are useful for treating inflammation,
 CC autoimmune diseases, cancer, cardiovascular disease, infections,
 CC rheumatoid arthritis, chronic inflammatory bowel disease, chronic
 CC inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis,
 CC atherosclerosis, psoriasis, rhinitis, and organ transplant rejection. The
 CC present amino acid sequence represents a chemokine analog peptide that
 CC was used in an example of the invention.

XX Sequence 31 AA;

Query Match 81.4%; Score 35; DB 9; Length 31;
 Best Local Similarity 77.8%; Pred. No. 8.7;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RSVLSYRF 9
 Db : |||||

1 KPVLSYRF 9

RESULT 13

ADY76973

ID ADY76973 standard; peptide; 26 AA.

XX ADY76973;

XX 02-JUN-2005 (first entry)

XX Chemokine analog peptide #62.

XX Chemokine; inflammation; antiinflammatory; autoimmune disease;
 KW immunosuppressive; cancer; cytostatic; cardiovascular disease;
 KW cardiovascular-gen.; infection; rheumatoid arthritis; antiarthritic;
 KW antirheumatic; chronic inflammatory bowel disease; antiinflammatory;
 KW gastrointestinal-gen.; multiple sclerosis; neuroprotective; asthma;
 KW antiasthmatic; osteoarthritis; osteopathic; atherosclerosis;
 KW antiarteriosclerotic; psoriasis; antipsoriatic; rhinitis; antiallergic;
 KW organ transplant rejection.

XX Synthetic.

OS Unidentified.

XX US2005059584-A1.

XX 17-MAR-2005.

OS Unidentified.

XX US2005059584-A1.

XX 17-MAR-2005.

XX 16-AUG-2002; 2002US-00222703.

XX 16-AUG-2002; 2002US-00222703.

XX (MERZ/) MERZOUK A.

PA (HABI/) HABI A.

PA (WONG/) WONG D.

PA (SALA/) SALARI H.

XX Merzouk A, Habi A, Wong D, Salari H;

PI WPI; 2005-232172/24.

XX Chemokine derived analog compound, useful for treating autoimmune
 PT diseases, chronic inflammation, cancer, cardiovascular disease, or
 PT infectious disease.

XX Example 17; Fig 17; 104pp; English.

XX The invention comprises chemokine derived analog peptides, such as
 CC stromal cell-derived factor-1 (SDF-1) peptides or macrophage inflammatory
 CC protein-1-alpha (MIP-1-alpha) peptides. The chemokine derived analog
 CC peptides of the invention are useful for treating inflammation,
 CC autoimmune diseases, cancer, cardiovascular disease, infections,
 CC rheumatoid arthritis, chronic inflammatory bowel disease, chronic
 CC inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis,
 CC atherosclerosis, psoriasis, rhinitis, and organ transplant rejection. The
 CC present amino acid sequence represents a chemokine analog peptide that
 CC was used in an example of the invention.

XX Sequence 26 AA;

Query Match 79.1%; Score 34; DB 9; Length 26;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 VLSYRF 9
 Db |||||

2 VLSYRF 8

RESULT 14

ADY77013

ID ADY77013 standard; peptide; 26 AA.

XX ADY77013;

XX 02-JUN-2005 (first entry)

XX Chemokine analog peptide #102.

XX Chemokine; inflammation; antiinflammatory; autoimmune disease;
 KW immunosuppressive; cancer; cytostatic; cardiovascular disease;
 KW cardiovascular-gen.; infection; rheumatoid arthritis; antiarthritic;
 KW antirheumatic; chronic inflammatory bowel disease; antiinflammatory;
 KW gastrointestinal-gen.; multiple sclerosis; neuroprotective; asthma;
 KW antiasthmatic; osteoarthritis; osteopathic; atherosclerosis;
 KW antiarteriosclerotic; psoriasis; antipsoriatic; rhinitis; antiallergic;
 KW organ transplant rejection.

XX Synthetic.

OS Unidentified.

XX US2005059584-A1.

XX 17-MAR-2005.

```

PF 16-AUG-2002; 2002US-00222703.
XX
PR 16-AUG-2002; 2002US-00222703.
XX
XX (MERZ/) MERZOUK A.
PA (HABI/) HABI A.
PA (WONG/) WONG D.
PA (SALA/) SALARI H.
XX
XX Merzouk A, Habi A, Wong D, Salari H;
XX
XX WPI; 2005-232172/24.
XX
XX Chemokine derived analog compound, useful for treating autoimmune
XX diseases, chronic inflammation, cancer, cardiovascular disease, or
XX infectious disease.
XX
XX Example 17; Fig 17; 104pp; English.
XX
XX The invention comprises chemokine derived analog peptides, such as
XX stromal cell-derived factor-1 (SDF-1) peptides or macrophage inflammatory
XX protein-1-alpha (MIP-1-alpha) peptides. The chemokine derived analog
XX peptides of the invention are useful for treating inflammation,
XX autoimmune diseases, cancer, cardiovascular disease, infections,
XX rheumatoid arthritis, chronic inflammatory bowel disease, chronic
XX inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis,
XX atherosclerosis, psoriasis, rhinitis, and organ transplant rejection. The
XX present amino acid sequence represents a chemokine analog peptide that
XX was used in an example of the invention.
XX
XX Sequence 26 AA;
SQ
Query Match 79.1%; Score 34; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 VLSLYRF 9
Db 2 VLSLYRF 8
|||||

RESULT 15
ADY77049
ID ADY77049 standard; peptide; 26 AA.
XX
XX ADY77049;
AC
XX
XX 02-JUN-2005 (first entry)
XX
XX Chemokine analog peptide #138.
XX
XX chemokine; inflammation; antiinflammatory; autoimmune disease;
XX immunosuppressive; cancer; cytostatic; cardiovascular disease;
XX cardiovascular-gen.; infection; rheumatoid arthritis; antiarthritis;
XX antirheumatic; chronic inflammatory bowel disease; antiinflammatory;
XX gastrointestinal-gen.; multiple sclerosis; neuroprotective; asthma;
XX antiasthmatic; osteoarthritis; osteopathic; atherosclerosis;
XX antiarteriosclerotic; psoriasis; antipsoriatic; rhinitis; antiallergic;
XX organ transplant rejection.
XX
XX Synthetic.
XX OS
XX Unidentified.
XX
XX US2005059584-A1.
XX
XX 17-MAR-2005.
XX
XX
XX 16-AUG-2002; 2002US-00222703.
XX
XX 16-AUG-2002; 2002US-00222703.
XX
XX (MERZ/) MERZOUK A.
XX PA (HABI/) HABI A.
XX

```

```

PA (WONG/) WONG D.
PA (SALA/) SALARI H.
XX
XX Merzouk A, Habi A, Wong D, Salari H;
XX
XX WPI; 2005-232172/24.
XX
XX Chemokine derived analog compound, useful for treating autoimmune
XX diseases, chronic inflammation, cancer, cardiovascular disease, or
XX infectious disease.
XX
XX Example 17; Fig 17; 104pp; English.
XX
XX The invention comprises chemokine derived analog peptides, such as
XX stromal cell-derived factor-1 (SDF-1) peptides or macrophage inflammatory
XX protein-1-alpha (MIP-1-alpha) peptides. The chemokine derived analog
XX peptides of the invention are useful for treating inflammation,
XX autoimmune diseases, cancer, cardiovascular disease, infections,
XX rheumatoid arthritis, chronic inflammatory bowel disease, chronic
XX inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis,
XX atherosclerosis, psoriasis, rhinitis, and organ transplant rejection. The
XX present amino acid sequence represents a chemokine analog peptide that
XX was used in an example of the invention.
XX
XX Sequence 26 AA;
SQ
Query Match 79.1%; Score 34; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 VLSLYRF 9
Db 2 VLSLYRF 8
|||||

Search completed: August 10, 2006, 23:00:39
Job time : 122.273 secs

```

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 10, 2006, 23:11:26 ; Search time 103.636 Seconds
(without alignments)
40.227 Million cell updates/sec

Title: US-10-825-603-5

Perfect score: 43

Sequence: 1 RSVSLSYRF 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	100.0	9	5	US-10-825-603-1
2	43	100.0	9	5	US-10-825-603-5
3	37	86.0	1356	6	US-11-129-741-2939
4	37	86.0	1356	6	US-11-129-741-2941
5	37	86.0	1356	6	US-11-129-741-2943
6	37	86.0	1356	6	US-11-129-741-2945
7	37	86.0	1356	6	US-11-129-741-2949
8	37	86.0	1356	6	US-11-129-741-2951
9	37	86.0	1356	6	US-11-129-741-4245
10	37	86.0	1362	5	US-10-895-064-420
11	37	86.0	1362	6	US-11-129-741-420
12	35	81.4	14	5	US-10-222-703A-831
13	35	81.4	14	5	US-10-222-703A-833
14	35	81.4	14	5	US-10-222-703A-855
15	35	81.4	14	5	US-10-222-703A-857
16	35	81.4	31	5	US-10-222-703A-830
17	35	81.4	31	5	US-10-222-703A-832
18	35	81.4	31	5	US-10-222-703A-854
19	35	81.4	31	5	US-10-222-703A-856
20	35	81.4	32	6	US-11-079-463-6615
21	34	79.1	55	4	US-10-437-963-188702
22	33	76.7	9	5	US-10-825-603-2
23	32	74.4	14	5	US-10-222-703A-847
24	32	74.4	14	5	US-10-222-703A-849
25	32	74.4	14	5	US-10-222-703A-851
26	32	74.4	14	5	US-10-222-703A-853
27	32	74.4	31	5	US-10-222-703A-846

28	32	74.4	31	5	US-10-222-703A-848	Sequence 848, App
29	32	74.4	31	5	US-10-222-703A-850	Sequence 850, App
30	32	74.4	31	5	US-10-222-703A-852	Sequence 852, App
31	32	74.4	53	4	US-10-437-963-135133	Sequence 135133,
32	32	74.4	271	4	US-10-029-386-33876	Sequence 33876, A
33	32	74.4	300	4	US-10-264-049-2346	Sequence 2346, Ap
34	32	74.4	396	4	US-10-094-749-2492	Sequence 2492, Ap
35	32	74.4	409	5	US-10-739-930-6621	Sequence 6621, Ap
36	32	74.4	445	4	US-10-104-047-2209	Sequence 2209, Ap
37	32	74.4	445	6	US-11-072-512-2209	Sequence 2209, Ap
38	32	74.4	569	4	US-10-115-482-38	Sequence 38, Appl
39	32	74.4	859	3	US-09-788-657-16	Sequence 16, Appl
40	32	74.4	859	3	US-09-912-697-4	Sequence 4, Appl
41	32	74.4	859	3	US-09-760-285-14	Sequence 14, Appl
42	32	74.4	859	4	US-10-270-839-25	Sequence 25, Appl
43	32	74.4	859	4	US-10-243-130-5	Sequence 5, Appl
44	32	74.4	859	4	US-10-371-634-3	Sequence 3, Appl
45	32	74.4	859	4	US-10-348-074-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1

US-10-825-603-1
; Sequence 1, Application US/10825603
; Publication No. US20050042635A1
; GENERAL INFORMATION:
; APPLICANT: THACKER, JAMES D.
; APPLICANT: FUHRER, PETER J.
; APPLICANT: WILLESFORD, KENNETH O.
; TITLE OF INVENTION: PROPHYLACTIC AND THERAPEUTIC BENEFITS OF A NEW CLASS OF
; FILE REFERENCE: IMMUNE STIMULATING PEPTIDES
; CURRENT FILING DATE: 2004-04-16
; PRIOR FILING DATE: 2003-04-16
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent in Ver. 3.2
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; FEATURE:
; OTHER INFORMATION: see specification as filed for preferred embodiments
US-10-825-603-1

Query Match 100.0%; Score 43; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RSVSLSYRF 9
Db 1 RSVSLSYRF 9

RESULT 2

US-10-825-603-5
; Sequence 5, Application US/10825603
; Publication No. US20050042635A1
; GENERAL INFORMATION:
; APPLICANT: THACKER, JAMES D.
; APPLICANT: FUHRER, PETER J.
; APPLICANT: WILLESFORD, KENNETH O.
; TITLE OF INVENTION: PROPHYLACTIC AND THERAPEUTIC BENEFITS OF A NEW CLASS OF
; FILE REFERENCE: IMMUNE STIMULATING PEPTIDES
; CURRENT FILING DATE: 2004-04-16
; PRIOR FILING DATE: 2003-04-16
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent in Ver. 3.2
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; FEATURE:
; OTHER INFORMATION: see specification as filed for preferred embodiments
US-10-825-603-1

; PRIOR APPLICATION NUMBER: 60/463,042
; PRIOR FILING DATE: 2003-04-16
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 5
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-825-603-5

Query Match 100.0%; Score 43; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSVLSYRF 9
||| |||||
DB 1 RSVLSYRF 9

RESULT 3

US-11-129-741-2939
; Sequence 2939, Application US/11129741
; Publication No. US20060034853A1
; GENERAL INFORMATION:
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: WOO, CHIU YAT PATRICK
; APPLICANT: LAU, KAR PUI SUSANNA
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: POON, LIT MAN
; APPLICANT: PEIRIS, JOSEPH S.M.
; APPLICANT: GUAN, YI
; TITLE OF INVENTION: A NOVEL HUMAN VIRUS CAUSING RESPIRATORY TRACT
; TITLE OF INVENTION: INFECTION AND USES THEREOF
; FILE REFERENCE: V0690.0044
; CURRENT APPLICATION NUMBER: US/11/129,741
; CURRENT FILING DATE: 2005-05-16
; PRIOR APPLICATION NUMBER: 10/895,064
; PRIOR FILING DATE: 2004-07-21
; NUMBER OF SEQ ID NOS: 4257
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2939
; LENGTH: 1356
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-129-741-2939

Query Match 86.0%; Score 37; DB 6; Length 1356;
Best Local Similarity 77.8%; Pred. No. 1.9e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RSVLSYRF 9
||| |||||
DB 760 RSISASYRF 768

RESULT 4

US-11-129-741-2941
; Sequence 2941, Application US/11129741
; Publication No. US20060034853A1
; GENERAL INFORMATION:
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: WOO, CHIU YAT PATRICK
; APPLICANT: LAU, KAR PUI SUSANNA
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: POON, LIT MAN
; APPLICANT: PEIRIS, JOSEPH S.M.
; APPLICANT: GUAN, YI
; TITLE OF INVENTION: A NOVEL HUMAN VIRUS CAUSING RESPIRATORY TRACT
; TITLE OF INVENTION: INFECTION AND USES THEREOF
; FILE REFERENCE: V0690.0044

; CURRENT APPLICATION NUMBER: US/11/129,741
; CURRENT FILING DATE: 2005-05-16
; PRIOR APPLICATION NUMBER: 10/895,064
; PRIOR FILING DATE: 2004-07-21
; NUMBER OF SEQ ID NOS: 4257
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2941
; LENGTH: 1356
; TYPE: PRT
; ORGANISM: Corononavirus-HKUI
US-11-129-741-2941

Query Match 86.0%; Score 37; DB 6; Length 1356;
Best Local Similarity 77.8%; Pred. No. 1.9e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RSVLSYRF 9
||| |||||
DB 760 RSISASYRF 768

RESULT 5

US-11-129-741-2943
; Sequence 2943, Application US/11129741
; Publication No. US20060034853A1
; GENERAL INFORMATION:
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: WOO, CHIU YAT PATRICK
; APPLICANT: LAU, KAR PUI SUSANNA
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: POON, LIT MAN
; APPLICANT: PEIRIS, JOSEPH S.M.
; APPLICANT: GUAN, YI
; TITLE OF INVENTION: A NOVEL HUMAN VIRUS CAUSING RESPIRATORY TRACT
; TITLE OF INVENTION: INFECTION AND USES THEREOF
; FILE REFERENCE: V0690.0044
; CURRENT APPLICATION NUMBER: US/11/129,741
; CURRENT FILING DATE: 2005-05-16
; PRIOR APPLICATION NUMBER: 10/895,064
; PRIOR FILING DATE: 2004-07-21
; NUMBER OF SEQ ID NOS: 4257
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2943
; LENGTH: 1356
; TYPE: PRT
; ORGANISM: Corononavirus-HKUI
US-11-129-741-2943

Query Match 86.0%; Score 37; DB 6; Length 1356;
Best Local Similarity 77.8%; Pred. No. 1.9e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RSVLSYRF 9
||| |||||
DB 760 RSISASYRF 768

RESULT 6

US-11-129-741-2945
; Sequence 2945, Application US/11129741
; Publication No. US20060034853A1
; GENERAL INFORMATION:
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: WOO, CHIU YAT PATRICK
; APPLICANT: LAU, KAR PUI SUSANNA
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: POON, LIT MAN
; APPLICANT: PEIRIS, JOSEPH S.M.
; APPLICANT: GUAN, YI
; TITLE OF INVENTION: A NOVEL HUMAN VIRUS CAUSING RESPIRATORY TRACT
; TITLE OF INVENTION: INFECTION AND USES THEREOF
; FILE REFERENCE: V0690.0044
; CURRENT APPLICATION NUMBER: US/11/129,741

; CURRENT FILING DATE: 2005-05-16
; PRIOR APPLICATION NUMBER: 10/895,064
; PRIOR FILING DATE: 2004-07-21
; NUMBER OF SEQ ID NOS: 4257
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2945
; LENGTH: 1356
; TYPE: PRT
; ORGANISM: Corononavirus-HKU1
US-11-129-741-2945

Query Match 86.0%; Score 37; DB 6; Length 1356;
Best Local Similarity 77.8%; Pred. No. 1.9e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RSVLSYRF 9
||:| ||||
DB 760 RSISASYRF 768

RESULT 7

US-11-129-741-2949
; Sequence 2949, Application US/11129741
; Publication No. US20060034853A1
; GENERAL INFORMATION:
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: WOO, CHIU YAT PATRICK
; APPLICANT: LAU, KAR PUI SUSANNA
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: POON, LIT MAN
; APPLICANT: PEIRIS, JOSEPH S.M.
; APPLICANT: GUAN, YI
; TITLE OF INVENTION: A NOVEL HUMAN VIRUS CAUSING RESPIRATORY TRACT
; FILE REFERENCE: V0690.0044
; CURRENT APPLICATION NUMBER: US/11/129,741
; PRIOR FILING DATE: 2005-05-16
; PRIOR APPLICATION NUMBER: 10/895,064
; PRIOR FILING DATE: 2004-07-21
; NUMBER OF SEQ ID NOS: 4257
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2949
; LENGTH: 1356
; TYPE: PRT
; ORGANISM: Corononavirus-HKU1
US-11-129-741-2949

Query Match 86.0%; Score 37; DB 6; Length 1356;
Best Local Similarity 77.8%; Pred. No. 1.9e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RSVLSYRF 9
||:| ||||
DB 760 RSISASYRF 768

RESULT 8

US-11-129-741-2951
; Sequence 2951, Application US/11129741
; Publication No. US20060034853A1
; GENERAL INFORMATION:
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: WOO, CHIU YAT PATRICK
; APPLICANT: LAU, KAR PUI SUSANNA
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: POON, LIT MAN
; APPLICANT: PEIRIS, JOSEPH S.M.
; APPLICANT: GUAN, YI
; TITLE OF INVENTION: A NOVEL HUMAN VIRUS CAUSING RESPIRATORY TRACT
; FILE REFERENCE: V0690.0044
; CURRENT APPLICATION NUMBER: US/11/129,741
; CURRENT FILING DATE: 2005-05-16

; PRIOR APPLICATION NUMBER: 10/895,064
; PRIOR FILING DATE: 2004-07-21
; NUMBER OF SEQ ID NOS: 4257
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2951
; LENGTH: 1356
; TYPE: PRT
; ORGANISM: Corononavirus-HKU1
US-11-129-741-2951

Query Match 86.0%; Score 37; DB 6; Length 1356;
Best Local Similarity 77.8%; Pred. No. 1.9e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RSVLSYRF 9
||:| ||||
DB 760 RSISASYRF 768

RESULT 9

US-11-129-741-4245
; Sequence 4245, Application US/11129741
; Publication No. US20060034853A1
; GENERAL INFORMATION:
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: WOO, CHIU YAT PATRICK
; APPLICANT: LAU, KAR PUI SUSANNA
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: POON, LIT MAN
; APPLICANT: PEIRIS, JOSEPH S.M.
; APPLICANT: GUAN, YI
; TITLE OF INVENTION: A NOVEL HUMAN VIRUS CAUSING RESPIRATORY TRACT
; FILE REFERENCE: V0690.0044
; CURRENT APPLICATION NUMBER: US/11/129,741
; PRIOR FILING DATE: 2005-05-16
; PRIOR APPLICATION NUMBER: 10/895,064
; PRIOR FILING DATE: 2004-07-21
; NUMBER OF SEQ ID NOS: 4257
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4245
; LENGTH: 1356
; TYPE: PRT
; ORGANISM: Corononavirus-HKU1
US-11-129-741-4245

Query Match 86.0%; Score 37; DB 6; Length 1356;
Best Local Similarity 77.8%; Pred. No. 1.9e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RSVLSYRF 9
||:| ||||
DB 760 RSISASYRF 768

RESULT 10

US-10-895-064-420
; Sequence 420, Application US/10895064
; Publication No. US20060018923A1
; GENERAL INFORMATION:
; APPLICANT: PEIRIS, JOSEPH S.M.
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: POON, LIT MAN
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: GUAN, YI
; APPLICANT: NICHOLLS, JOHN M.
; APPLICANT: LEUNG, FREDERICK C.
; TITLE OF INVENTION: A NOVEL HUMAN VIRUS CAUSING RESPIRATORY TRACT INFECTION AND USES
; FILE REFERENCE: V0690.0031
; CURRENT APPLICATION NUMBER: US/10/895,064
; CURRENT FILING DATE: 2004-07-21
; NUMBER OF SEQ ID NOS: 2918

; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 420
; LENGTH: 1362
; TYPE: PRT
; ORGANISM: Corononavirus-HKU1
US-10-895-084-420

Query Match 86.0%; Score 37; DB 5; Length 1362;
Best Local Similarity 77.8%; Pred. No. 1.9e+02;
Matches 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RSVLSYRPF 9
|||:|||||
Db 766 RSISASYRPF 774

RESULT 11

US-11-129-741-420
; Sequence 420, Application US/11129741
; Publication No. US20060034853A1

; GENERAL INFORMATION:

; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: WOO, CHIU YAT PATRICK
; APPLICANT: LAU, KAR PUI SUSANNA
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: POON, LIT MAN
; APPLICANT: PEIRIS, JOSEPH S.M.
; APPLICANT: GUAN, YI

; TITLE OF INVENTION: A NOVEL HUMAN VIRUS CAUSING RESPIRATORY TRACT

; FILE REFERENCE: INFECTION AND USES THEREOF

; CURRENT APPLICATION NUMBER: US/11/129,741

; CURRENT FILING DATE: 2005-05-16

; PRIOR APPLICATION NUMBER: 10/895,064

; PRIOR FILING DATE: 2004-07-21

; NUMBER OF SEQ ID NOS: 4257

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 420

; LENGTH: 1362

; TYPE: PRT

; ORGANISM: Corononavirus-HKU1

US-11-129-741-420

Query Match 86.0%; Score 37; DB 6; Length 1362;
Best Local Similarity 77.8%; Pred. No. 1.9e+02;
Matches 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RSVLSYRPF 9
|||:|||||
Db 766 RSISASYRPF 774

RESULT 12

US-10-222-703A-831
; Sequence 831, Application US/10222703A
; Publication No. US20050059584A1

; GENERAL INFORMATION:

; APPLICANT: MERZOUK, AHMED
; APPLICANT: HABI, ABDELKRIM
; APPLICANT: WONG, DONALD
; APPLICANT: SALARI, HASSAN

; TITLE OF INVENTION: NOVEL CHEMOKINE MIMETICS SYNTHESIS AND THEIR USE

; FILE REFERENCE: 592960-00002

; CURRENT APPLICATION NUMBER: US/10/222,703A

; CURRENT FILING DATE: 2002-08-16

; PRIOR APPLICATION NUMBER: 10/086,177

; PRIOR FILING DATE: 2002-02-26

; PRIOR APPLICATION NUMBER: 09/835,107

; PRIOR FILING DATE: 2001-04-12

; PRIOR APPLICATION NUMBER: 60/373,629

; PRIOR FILING DATE: 2002-04-17

; PRIOR APPLICATION NUMBER: 60/373,628

; PRIOR FILING DATE: 2002-04-17

; NUMBER OF SEQ ID NOS: 868
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 831
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-222-703A-831

Query Match 81.4%; Score 35; DB 5; Length 14;
Best Local Similarity 77.8%; Pred. No. 3.9;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RSVLSYRPF 9
:|||||||
Db 1 KPVLSYRPF 9

RESULT 13

US-10-222-703A-833

; Sequence 833, Application US/10222703A

; Publication No. US20050059584A1

; GENERAL INFORMATION:

; APPLICANT: MERZOUK, AHMED
; APPLICANT: HABI, ABDELKRIM
; APPLICANT: WONG, DONALD
; APPLICANT: SALARI, HASSAN

; TITLE OF INVENTION: NOVEL CHEMOKINE MIMETICS SYNTHESIS AND THEIR USE

; FILE REFERENCE: 592960-00002

; CURRENT APPLICATION NUMBER: US/10/222,703A

; CURRENT FILING DATE: 2002-08-16

; PRIOR APPLICATION NUMBER: 10/086,177

; PRIOR FILING DATE: 2002-02-26

; PRIOR APPLICATION NUMBER: 09/835,107

; PRIOR FILING DATE: 2001-04-12

; PRIOR APPLICATION NUMBER: 60/373,629

; PRIOR FILING DATE: 2002-04-17

; PRIOR APPLICATION NUMBER: 60/373,628

; PRIOR FILING DATE: 2002-04-17

; NUMBER OF SEQ ID NOS: 868

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 833

; LENGTH: 14

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic peptide

; FEATURE:

; NAME/KEY: MOD_RES

; LOCATION: (2)..(2)

; OTHER INFORMATION: D-Pro

; FEATURE:

; NAME/KEY: MOD_RES

; LOCATION: (5)..(5)

; OTHER INFORMATION: D-Leu

US-10-222-703A-833

Query Match 81.4%; Score 35; DB 5; Length 14;
Best Local Similarity 77.8%; Pred. No. 3.9;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RSVLSYRPF 9
:|||||||
Db 1 KPVLSYRPF 9

RESULT 14

US-10-222-703A-855

; Sequence 855, Application US/10222703A

; Publication No. US20050059584A1

; GENERAL INFORMATION:

; APPLICANT: MERZOUK, AHMED

; APPLICANT: HABI, ABDELKRIM
; APPLICANT: WONG, DONALD
; APPLICANT: SALARI, HASSAN
; TITLE OF INVENTION: NOVEL CHEMOKINE MIMETICS SYNTHESIS AND THEIR USE
; FILE REFERENCE: 592960-00002
; CURRENT APPLICATION NUMBER: US/10/222,703A
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: 10/086,177
; PRIOR FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: 09/835,107
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/373,629
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/373,628
; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 868
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 855
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-222-703A-855

Query Match 81.4%; Score 35; DB 5; Length 14;
Best Local Similarity 77.8%; Pred. No. 3.9;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RSVLSYRF 9
: |||||
Db 1 KPVLSYRF 9

RESULT 15
US-10-222-703A-857
; Sequence 857, Application US/10222703A
; Publication No. US20050059584A1
; GENERAL INFORMATION:
; APPLICANT: MERZOUK, AHMED
; APPLICANT: HABI, ABDELKRIM
; APPLICANT: WONG, DONALD
; APPLICANT: SALARI, HASSAN
; TITLE OF INVENTION: NOVEL CHEMOKINE MIMETICS SYNTHESIS AND THEIR USE
; FILE REFERENCE: 592960-00002
; CURRENT APPLICATION NUMBER: US/10/222,703A
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: 10/086,177
; PRIOR FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: 09/835,107
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/373,629
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/373,628
; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 868
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 857
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; NAME/KEY: MOD RES
; LOCATION: (2)..(2)
; OTHER INFORMATION: D-Pro
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (5)..(5)
; OTHER INFORMATION: D-Leu
US-10-222-703A-857

Query Match 81.4%; Score 35; DB 5; Length 14;
Best Local Similarity 77.8%; Pred. No. 3.9;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 RSVLSYRF 9
: |||||
Db 1 KPVLSYRF 9

Search completed: August 10, 2006, 23:19:37
Job time : 104.636 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 10, 2006, 23:13:31 ; Search time 16.3636 Seconds
37.022 Million cell updates/sec
(without alignments)

Title: US-10-825-603-5

Perfect score: 43

Sequence: 1 RSVSLSVRF 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 239914 seqs, 67312017 residues

Total number of hits satisfying chosen parameters: 239914

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA New:
1: /EMC_Celerra_SID83/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
2: /EMC_Celerra_SID83/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
3: /EMC_Celerra_SID83/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
4: /EMC_Celerra_SID83/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
5: /EMC_Celerra_SID83/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
6: /EMC_Celerra_SID83/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
7: /EMC_Celerra_SID83/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
8: /EMC_Celerra_SID83/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	72.1	372	7 US-11-056-355B-81312	Sequence 81312, A
2	31	72.1	439	7 US-11-056-355B-81311	Sequence 81311, A
3	31	72.1	441	7 US-11-056-355B-81310	Sequence 81310, A
4	31	72.1	483	7 US-11-330-403-16842	Sequence 16842, A
5	31	72.1	484	7 US-11-330-403-4463	Sequence 4463, A
6	31	72.1	484	7 US-11-330-403-5632	Sequence 5632, A
7	31	72.1	484	7 US-11-330-403-7972	Sequence 7972, A
8	31	72.1	484	7 US-11-330-403-8319	Sequence 8319, A
9	31	72.1	484	7 US-11-330-403-18291	Sequence 18291, A
10	30	69.8	262	6 US-10-953-349-10285	Sequence 10285, A
11	30	69.8	262	7 US-11-056-355B-49774	Sequence 49774, A
12	30	69.8	262	7 US-11-056-355B-88515	Sequence 88515, A
13	30	69.8	262	7 US-11-056-355B-92271	Sequence 92271, A
14	30	69.8	282	6 US-10-953-349-10284	Sequence 10284, A
15	30	69.8	282	7 US-11-056-355B-49773	Sequence 49773, A
16	30	69.8	282	7 US-11-056-355B-88514	Sequence 88514, A
17	30	69.8	282	7 US-11-056-355B-92270	Sequence 92270, A
18	30	69.8	283	6 US-10-953-349-10283	Sequence 10283, A
19	30	69.8	283	7 US-11-056-355B-49772	Sequence 49772, A
20	30	69.8	283	7 US-11-056-355B-88513	Sequence 88513, A
21	30	69.8	283	7 US-11-056-355B-92269	Sequence 92269, A
22	30	69.8	568	7 US-11-233-089-2	Sequence 2, Appli
23	30	69.8	568	7 US-11-233-089-4	Sequence 4, Appli
24	30	69.8	942	6 US-10-449-902-52959	Sequence 52959, A
25	30	69.8	981	6 US-10-449-902-41190	Sequence 41190, A

26 29 67.4 73 6 US-10-196-749-396 Sequence 396, App
27 29 67.4 73 7 US-11-101-316-148 Sequence 148, App
28 29 67.4 73 7 US-11-376-673-148 Sequence 148, App
29 29 67.4 79 7 US-11-056-355B-21714 Sequence 21714, A
30 29 67.4 93 6 US-10-505-928-112 Sequence 112, App
31 29 67.4 93 6 US-10-511-937-2454 Sequence 2454, App
32 29 67.4 138 7 US-11-056-355B-107948 Sequence 107948, App
33 29 67.4 138 7 US-11-056-355B-107947 Sequence 107947, App
34 29 67.4 147 7 US-11-056-355B-107947 Sequence 107947, App
35 29 67.4 147 7 US-11-056-355B-119186 Sequence 119186, App
36 29 67.4 429 7 US-11-330-403-8035 Sequence 8035, App
37 29 67.4 458 7 US-11-317-571-147 Sequence 147, App
38 29 67.4 483 6 US-10-449-902-44566 Sequence 44566, A
39 29 67.4 499 7 US-11-317-789A-221 Sequence 221, App
40 29 67.4 526 7 US-11-056-355B-87100 Sequence 87100, A
41 29 67.4 527 7 US-11-056-355B-87012 Sequence 87012, A
42 29 67.4 546 7 US-11-056-355B-87099 Sequence 87099, A
43 29 67.4 547 7 US-11-056-355B-87011 Sequence 87011, A
44 29 67.4 595 7 US-11-056-355B-87098 Sequence 87098, A
45 29 67.4 596 7 US-11-056-355B-69860 Sequence 69860, A

ALIGNMENTS

RESULT 1
US-11-056-355B-81312
; Sequence 81312, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 81312
; LENGTH: 372
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(372)
; OTHER INFORMATION: Ceres Seq. ID no. 12659264
US-11-056-355B-81312

Query Match 72.1%; Score 31; DB 7; Length 372;
Best Local Similarity 75.0%; Pred. No. 75;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSVSLSVR 8
DB 318 RSVSLSVR 325

RESULT 2
US-11-056-355B-81311
; Sequence 81311, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13

```

; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 81311
; LENGTH: 439
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(439)
; OTHER INFORMATION: Ceres Seq. ID no. 12659263
US-11-056-355B-81311

Query Match      72.1%; Score 31; DB 7; Length 439;
Best Local Similarity 75.0%; Pred. No. 90;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 RSVSLSYR 8
Db      385 RSVSISYQ 392
|||||:|:|

RESULT 3
US-11-056-355B-81310
; Sequence 81310, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 81310
; LENGTH: 441
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(441)
; OTHER INFORMATION: Ceres Seq. ID no. 12659262
US-11-056-355B-81310

Query Match      72.1%; Score 31; DB 7; Length 441;
Best Local Similarity 75.0%; Pred. No. 90;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 RSVSLSYR 8
Db      387 RSVSISYQ 394
|||||:|:|

RESULT 4
US-11-330-403-16842
; Sequence 16842, Application US/11330403
; Publication No. US20060159563A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53629)B
; CURRENT APPLICATION NUMBER: US/11/330,403
; CURRENT FILING DATE: 2006-01-12
; NUMBER OF SEQ ID NOS: 19250
; SEQ ID NO 16842
; LENGTH: 483
; TYPE: prt
; ORGANISM: Proteus mirabilis
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(483)
; OTHER INFORMATION: unsure at all xaa locations
US-11-330-403-16842

Query Match      72.1%; Score 31; DB 7; Length 483;
Best Local Similarity 66.7%; Pred. No. 99;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 RSVSLSYR 9
Db      181 RGLPLSYRF 189
|||||:|:|

RESULT 5
US-11-330-403-4463
; Sequence 4463, Application US/11330403
; Publication No. US20060159563A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53629)B
; CURRENT APPLICATION NUMBER: US/11/330,403
; CURRENT FILING DATE: 2006-01-12
; NUMBER OF SEQ ID NOS: 19250
; SEQ ID NO 4463
; LENGTH: 484
; TYPE: prt
; ORGANISM: Proteus mirabilis
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(484)
; OTHER INFORMATION: unsure at all xaa locations
US-11-330-403-4463

Query Match      72.1%; Score 31; DB 7; Length 484;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 RSVSLSYR 9
Db      182 RGLPLSYRF 190
|||||:|:|

RESULT 6
US-11-330-403-5632
; Sequence 5632, Application US/11330403
; Publication No. US20060159563A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53629)B
; CURRENT APPLICATION NUMBER: US/11/330,403
; CURRENT FILING DATE: 2006-01-12
; NUMBER OF SEQ ID NOS: 19250
; SEQ ID NO 5632
; LENGTH: 484
; TYPE: prt
; ORGANISM: Proteus mirabilis
US-11-330-403-5632

Query Match      72.1%; Score 31; DB 7; Length 484;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 RSVSLSYR 9
Db      182 RGLPLSYRF 190
|||||:|:|

RESULT 7
US-11-330-403-7972
; Sequence 7972, Application US/11330403
; Publication No. US20060159563A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.

```

; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53629)B
; CURRENT APPLICATION NUMBER: US/11/330,403
; CURRENT FILING DATE: 2006-01-12
; NUMBER OF SEQ ID NOS: 19250
; SEQ ID NO 7972
; LENGTH: 484
; TYPE: PRT
; ORGANISM: Proteus mirabilis
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(484)
; OTHER INFORMATION: unsure at all Xaa locations
US-11-330-403-7972

Query Match 72.1%; Score 31; DB 7; Length 484;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RSVLSYRF 9
| : |||||
Db 182 RGLPLSYRF 190

RESULT 8

US-11-330-403-8319
; Sequence 8319, Application US/11330403
; Publication No. US20060159563A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53629)B
; CURRENT APPLICATION NUMBER: US/11/330,403
; CURRENT FILING DATE: 2006-01-12
; NUMBER OF SEQ ID NOS: 19250
; SEQ ID NO 8319
; LENGTH: 484
; TYPE: PRT
; ORGANISM: Proteus mirabilis
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(484)
; OTHER INFORMATION: unsure at all Xaa locations
US-11-330-403-8319

Query Match 72.1%; Score 31; DB 7; Length 484;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RSVLSYRF 9
| : |||||
Db 182 RGLPLSYRF 190

RESULT 9

US-11-330-403-18291
; Sequence 18291, Application US/11330403
; Publication No. US20060159563A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53629)B
; CURRENT APPLICATION NUMBER: US/11/330,403
; CURRENT FILING DATE: 2006-01-12
; NUMBER OF SEQ ID NOS: 19250
; SEQ ID NO 18291
; LENGTH: 484
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-11-330-403-18291

Query Match 72.1%; Score 31; DB 7; Length 484;
Best Local Similarity 66.7%; Pred. No. 1e+02;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 RSVLSYRF 9
| : |||||
Db 182 RGLPLSYRF 190

RESULT 10

US-10-953-349-10285
; Sequence 10285, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10285
; LENGTH: 262
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-10285

Query Match 69.8%; Score 30; DB 6; Length 262;
Best Local Similarity 66.7%; Pred. No. 84;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RSVLSYRF 9
| : |||||
Db 174 RSSSLAFRF 182

RESULT 11

US-11-056-355B-49774
; Sequence 49774, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119666
; SEQ ID NO 49774
; LENGTH: 262
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(262)
; OTHER INFORMATION: Ceres Seq. ID no. 13648120
US-11-056-355B-49774

Query Match 69.8%; Score 30; DB 7; Length 262;
Best Local Similarity 66.7%; Pred. No. 84;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RSVLSYRF 9
| : |||||
Db 174 RSSSLAFRF 182

RESULT 12

US-11-056-355B-88515
; Sequence 88515, Application US/11056355B
; Publication No. US20060150283A1

```
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 88515
; LENGTH: 262
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(262)
; OTHER INFORMATION: Ceres Seq. ID no. 12710126
US-11-056-355B-88515

Query Match      69.8%; Score 30; DB 7; Length 262;
Best Local Similarity 66.7%; Pred. No. 84;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RSVLSYRF 9
Db 174 RSSSLAFRF 182

RESULT 13
US-11-056-355B-92271
; Sequence 92271, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 92271
; LENGTH: 262
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(262)
; OTHER INFORMATION: Ceres Seq. ID no. 12710126
US-11-056-355B-92271

Query Match      69.8%; Score 30; DB 7; Length 262;
Best Local Similarity 66.7%; Pred. No. 84;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RSVLSYRF 9
Db 174 RSSSLAFRF 182

RESULT 14
US-10-953-349-10284
; Sequence 10284, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
```

```
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10284
; LENGTH: 282
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-10284

Query Match      69.8%; Score 30; DB 6; Length 282;
Best Local Similarity 66.7%; Pred. No. 91;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RSVLSYRF 9
Db 194 RSSSLAFRF 202

RESULT 15
US-11-056-355B-49773
; Sequence 49773, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 49773
; LENGTH: 282
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(282)
; OTHER INFORMATION: Ceres Seq. ID no. 13648119
US-11-056-355B-49773

Query Match      69.8%; Score 30; DB 7; Length 282;
Best Local Similarity 66.7%; Pred. No. 91;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RSVLSYRF 9
Db 194 RSSSLAFRF 202

Search completed: August 10, 2006, 23:20:43
Job time : 17.3636 secs
```

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 10, 2006, 22:53:25 ; Search time 150 Seconds
(without alignments)
55.501 Million cell updates/sec

Title: US-10-825-603-1

Perfect score: 43

Sequence: 1 RSVLSLYRF 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 7.2.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	37	86.0	350	Q2RSU4_RHORU	Q2rsu4 rhodospiril
2	37	86.0	1356	Q5MQD0_9COCO	Q5mqd0 human coron
3	35	81.4	165	Q9LSS1_ARATH	Q9lss1 arabidopsis
4	35	81.4	218	Q34VG2_9GAMM	Q34vg2 alkaliilmi
5	35	81.4	322	Q5EGW8_9POXV	Q5egw8 goatpox vir
6	35	81.4	468	Q23425_ARATH	Q23425 arabidopsis
7	35	81.4	1125	Q5LQZ9_BACFN	Q5ldz9 bacteroides
8	35	81.4	1125	Q93TH9_BACFR	Q93th9 bacteroides
9	34	79.1	333	Q3GT18_9DELT	Q3gt18 pelobacter
10	34	79.1	366	Q6D6D4_ERWCT	Q6dd64 erwinia car
11	34	79.1	367	Q9RM69_ERWCA	Q9rm69 erwinia car
12	34	79.1	372	Q4BP04_BURVI	Q4bp04 burkholderi
13	34	79.1	403	Q96773_HAEDU	Q96773 haemophilus
14	34	79.1	433	Q2S253_9SPHI	Q2s253 salinibacte
15	34	79.1	559	Q9DQ91_9CLOS	Q9dq91 pineapple m
16	34	79.1	705	Q4Q9U3_LEIMA	Q4q9u3 leishmania
17	34	79.1	932	Q2R0G4_ORYSA	Q2r0g4 oryza sativ
18	34	79.1	6733	Q3T8J2_9NIDO	Q3t8j2 breda virus
19	33	76.7	154	Q6MAQ2_PARUM	Q6maq2 parachlamyd
20	33	76.7	282	Q6CYK2_ERWCT	Q6cyk2 erwinia car
21	33	76.7	299	Q9RBF7_RALEU	Q9rbf7 ralstonia e
22	33	76.7	387	Q7QBV3_ANOGA	Q7qbv3 anopheles g
23	33	76.7	391	Q8DTD9_STRMU	Q8dtd9 streptococc
24	33	76.7	405	Q6PRG7_CANGA	Q6fgr7 candida gla
25	33	76.7	456	Q3CKF4_THETP	Q3ckf4 thermoplas
26	33	76.7	505	Q5L215_GEOKA	Q5l215 geobacillus
27	33	76.7	652	Q3P7X1_PARDP	Q3p7x1 paracoccus
28	33	76.7	720	Q582S8_9TRYP	Q582s8 trypanosoma
29	33	76.7	756	Q2UL42_ASPOR	Q2ul42 aspergillus
30	33	76.7	757	Q5B3B3_EMENI	Q5b3b3 aspergillus
31	33	76.7	777	Q9ZS42_LYCPS	Q9zs42 lycopersico

32 33 76.7 811 2 Q89Z09_BACTN Q89z09 bacteroides
33 33 76.7 904 2 Q6AIG9_DESPS Q6aig9 desulfocale
34 33 76.7 1310 2 Q8A084_BACTN Q8a084 bacteroides
35 33 76.7 16311 2 Q3AR72_CHLCH Q3ar72 chlorobium
36 32 74.4 80 2 Q4XYD5_PLACH Q4xyd5 plasmodium
37 32 74.4 147 2 Q93QN1_9ENTR Q93qn1 brenneria s
38 32 74.4 147 2 Q93QN2_9ENTR Q93qn2 brenneria s
39 32 74.4 147 2 Q93QN6_9ENTR Q93qn6 brenneria s
40 32 74.4 150 2 Q4HSF7_CAMUP Q4hsf7 campylobact
41 32 74.4 157 2 Q8D9U8_VIBUQ Q8d9u8 vibrio vuln
42 32 74.4 163 2 Q8CDH0_MOUSE Q8cdh0 mus musculu
43 32 74.4 170 2 Q2IYR9_RHOPA Q2iyr9 rhodopsedu
44 32 74.4 180 2 Q6N3U4_RHOPA Q6n3u4 rhodopsedu
45 32 74.4 180 2 Q8XYV4_RALSO Q8xyv4 ralstonia s

ALIGNMENTS

RESULT 1
Q2RSU4_RHORU PRELIMINARY; PRT; 350 AA.
AC Q2RSU4;
DT 24-JAN-2006, integrated into UniprotKB/TrEMBL.
DT 24-JAN-2006, sequence version 1.
DT 07-FEB-2006, entry version 2.
DE Hypothetical protein precursor.
GN ORFNames=Rru_A2001;
OS Rhodospirillum rubrum ATCC 11170.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
OC Rhodospirillaceae; Rhodospirillum.
OX NCBI_TaxID=269796;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 11170;
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler J.C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Munk A.C., Brettin T., Bruce D.,
RA Han C., Tapia R., Gilna P., Schmutz J., Larimer F., Land M.,
RA Kyrpides N., Mavromatis K., Richardson P., Zhang Y., Roberts G.,
RA Reslewic S., Zhou S., Schwartz D.C.;
RT "Complete sequence of the chromosome of Rhodospirillum rubrum ATCC
11170.";
RL Submitted (DEC-2005) to the EMBL/GenBank/DBJ databases.
CC -----
CC Copyrighted by the Uniprot Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; CP000230; ABC22801.1; -; Genomic_DNA.
KW Hypothetical protein; Signal.
FT SIGNAL 1 26
SQ SEQUENCE 350 AA; 5FB0C4570E989D7 CRC64;
Query Match 86.0%; Score 37; DB 2; Length 350;
Best Local Similarity 87.5%; Pred. No. 22;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SVLSLYRF 9
Db 343 SISLSLYRF 350

RESULT 2
Q5MQD0_9COCO PRELIMINARY; PRT; 1356 AA.
AC Q5MQD0;
DT 01-FEB-2005, integrated into UniprotKB/TrEMBL.
DT 01-FEB-2005, sequence version 1.
DT 21-FEB-2006, entry version 6.
DE Spike glycoprotein.
GN Name=S; ORFNames=HCHV1gp3;
OS Human coronavirus HKU1.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus; Group 2 species;

```

OC unclassified Group 2 species.
OX NCBI_TaxID=290028;
RN
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HKU1;
RX PubMed=15613317; DOI=10.1128/JVI.79.2.884-895.2005;
RA Woo P.C., Lau S.K., Chu C.M., Chan K.H., Tsoi H.W., Huang Y.,
RA Wong B.H., Poon R.W., Cai J.J., Luk W.K., Poon L.L., Wong S.S.,
RA Guan Y., Peiris J.S., Yuen K.Y.;
RT "Characterization and complete genome sequence of a novel coronavirus,
RL coronavirus HKU1, from patients with pneumonia.";
RL J. Virol. 79:884-895(2005).
RN
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HKU1;
RA Woo P.C.Y., Lau S.K.P., Chan K.H., Tsoi H.W., Huang Y., Wong B.H.L.,
RA Cai J.J., Wong S.S.Y., Peiris J.S.M., Chu C.M., Yuen K.Y.;
RL Submitted (JAN-2006) to the EMBL/GenBank/DBJ databases.
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AY597011; AAT98580.1; -; Genomic RNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0006944; P:membrane fusion; IEA.
DR GO; GO:0046813; P:viral attachment, binding of host cell sur. . .; IEA.
DR InterPro; IPR002552; Corona_S2.
DR Pfam; PF01601; Corona_S2; 1.
SQ SEQUENCE 1356 AA; 151711 MW; EE319676930C844E CRC64;

Query Match 86.0%; Score 37; DB 2; Length 1356;
Best Local Similarity 77.8%; Pred. No. 99;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RSVSLSYRF 9
||:|||||
Db 760 RSISASYRF 768

RESULT 3
Q9LS1 ARATH PRELIMINARY; PRT; 165 AA.
AC Q9LS1;
DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2000, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE Arabidopsis thaliana genomic DNA, chromosome 5, BAC clone: F15L12.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Kaneko T., Katoh T., Asamizu E., Sato S., Nakamura Y., Kotani H.,
RA Tabata S.;
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AB026632; BAA97506.1; -; Genomic DNA.
SQ SEQUENCE 165 AA; 18500 MW; 8BBF132B3DD184 CRC64;

Query Match 81.4%; Score 35; DB 2; Length 165;
Best Local Similarity 87.5%; Pred. No. 26;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SVLSYRF 9
|:|||||
Db 158 SLSYRF 165

RESULT 4
Q34VG2 9GAMM PRELIMINARY; PRT; 218 AA.
ID Q34VG2_9GAMM
AC Q34VG2;
DT 06-DEC-2005, integrated into UniProtKB/TrEMBL.
DT 06-DEC-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Hypothetical protein precursor.
GN ORFNames=MIGRORAF1_0253;
OS Alkalilimnicola ehrlichei MLHE-1.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Chromatiales;
OC Ectothiorhodospiraceae; Alkalilimnicola.
OX NCBI_TaxID=187272;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=MLHE-1;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T.,
RA Hammon N., Izrani S., Pittluck S., Richardson P.;
RT "Sequencing of the draft genome and assembly of Alkalilimnicola
RT ehrlichei MLHE-1.";
RL Submitted (OCT-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=MLHE-1;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome of Alkalilimnicola ehrlichei MLHE-1.";
RL Submitted (NOV-2005) to the EMBL/GenBank/DBJ databases.
CC
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AALK0100027; EAP33167.1; -; Genomic DNA.
KW Hypothetical protein; Signal.
FT SIGNAL 1 26 Potential.
SQ SEQUENCE 218 AA; 23556 MW; 739FCA2B0C70C1FE CRC64;

Query Match 81.4%; Score 35; DB 2; Length 218;
Best Local Similarity 87.5%; Pred. No. 36;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SVLSYRF 9
||:|||||
Db 211 SVALSYRF 218

RESULT 5
Q5EGW8 9POXV PRELIMINARY; PRT; 322 AA.
ID Q5EGW8_9POXV
AC Q5EGW8;
DT 15-MAR-2005, integrated into UniProtKB/TrEMBL.
DT 15-MAR-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE P32.
OS Goatpox virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Capripoxvirus.
OX NCBI_TaxID=186805;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Guo W.;
RT "Cloning and Expression of Capripoxvirus P32 Gene.";
RL Thesis (2004), Northeast Agriculture University, No.50, St. Mucai,
RL Harbin, Heilongjiang, People's Republic of China.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Guo W., Qu J., Xiang W., Li Y.;
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.

```

```

CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AY981707; AAW78648.1; -; mRNA.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR InterPro; IPR004900; Pox_P35.
DR Pfam; PF03213; Pox_P35; 1.
DR SQU SEQUENCE 322 AA; 37559 MW; DC141BC26162CB7B CRC64;

Query Match 81.4%; Score 35; DB 2; Length 322;
Best Local Similarity 66.7%; Pred. No. 55;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RVSLSYRF 9
DB 53 KDISLSYRF 61

RESULT 6
O23425 ARATH PRELIMINARY; PRT; 468 AA.
AC O23425;
DT 01-JAN-1998, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 1.
DE DNA chromosome 4, ESSA 1 CONTIG fragment NO. 4 (Hypothetical protein
AT4g15740).
GN Names:AT4G15740; Synonyms:AT4G15740; OrderedLocusNames=At4g15740;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC Rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OC NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Bevan M., Stiekema W., Murphy G., Wambutt R., Pohl T., Terry N.,
RA Kreis M., Kavanagh T., Etian K.D., Rieger M., James R.,
RA Puigdomenech P., Hatzipoulos P., Obermaier B., Duesterhoft A.,
RA Jones J., Palme C., Ansoorge W., Delseny M., Bancroft I., Mewes H.W.,
RA Schueller C., Chalwatzi N.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 2 C2 domains.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; Z97339; CAB10352.1; -; Genomic DNA.
DR EMBL; AL161542; CAB78616.1; -; Genomic DNA.
DR PIR; F71422; F71422.
DR TAIR; At4g15740.
DR InterPro; IPR000008; C2.
DR InterPro; IPR002052; N6_Mtase.
DR Pfam; PF00168; C2; 2.
DR SMART; SM00239; C2; 2.
DR PROSITE; PS50004; C2 DOMAIN; 1.
DR PROSITE; PS00092; N6_MTASE; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 468 AA; 52292 MW; EF0035F3536D7877 CRC64;

Query Match 81.4%; Score 35; DB 2; Length 468;
Best Local Similarity 87.5%; Pred. No. 84;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SVLSYRF 9
DB 174 TVLSYRF 181

RESULT 7
O23425 ARATH PRELIMINARY; PRT; 468 AA.
AC O23425;
DT 01-JAN-1998, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 1.
DE DNA chromosome 4, ESSA 1 CONTIG fragment NO. 4 (Hypothetical protein
AT4g15740).
GN Names:AT4G15740; Synonyms:AT4G15740; OrderedLocusNames=At4g15740;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC Rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OC NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Bevan M., Stiekema W., Murphy G., Wambutt R., Pohl T., Terry N.,
RA Kreis M., Kavanagh T., Etian K.D., Rieger M., James R.,
RA Puigdomenech P., Hatzipoulos P., Obermaier B., Duesterhoft A.,
RA Jones J., Palme C., Ansoorge W., Delseny M., Bancroft I., Mewes H.W.,
RA Schueller C., Chalwatzi N.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 2 C2 domains.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; Z97339; CAB10352.1; -; Genomic DNA.
DR EMBL; AL161542; CAB78616.1; -; Genomic DNA.
DR PIR; F71422; F71422.
DR TAIR; At4g15740.
DR InterPro; IPR000008; C2.
DR InterPro; IPR002052; N6_Mtase.
DR Pfam; PF00168; C2; 2.
DR SMART; SM00239; C2; 2.
DR PROSITE; PS50004; C2 DOMAIN; 1.
DR PROSITE; PS00092; N6_MTASE; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 468 AA; 52292 MW; EF0035F3536D7877 CRC64;

Query Match 81.4%; Score 35; DB 2; Length 1125;
Best Local Similarity 66.7%; Pred. No. 22e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RVSLSYRF 9
DB 1051 REITLSYRF 1059

RESULT 8
Q93TH9 BACFR PRELIMINARY; PRT; 1125 AA.
AC Q93TH9;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 1.
DE Outer membrane protein Omp121.
GN OrderedLocusNames=BF1894;
OS Bacteroides fragilis.
OC Bacteria; Bacteroidetes; Bacteroidetes (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OC NCBI_TaxID=817;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC25285;
RX MEDLINE=21856486; PubMed=11867216; DOI=10.1016/S0378-1119(01)00835-6;
RA Wexler H.M., Read E.K., Tomzynski T.J.;
RT "Characterization of omp200, a porin gene complex from Bacteroides
fragilis: omp121 and omp71, gene sequence, deduced amino acid
sequences and predictions of porin structure.";
RL Gene 283:95-105(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=YCH46;
RX PubMed=15466707; DOI=10.1073/pnas.0404172101;
RA Kuwahara T., Yamashita A., Hirakawa H., Nakayama H., Toh H., Okada N.,
RA Kuhara S., Hattori M., Hayaishi T., Ohnishi Y.;

```

```

RESULT 7
Q5LDZ9_BACFN PRELIMINARY; PRT; 1125 AA.
ID Q5LDZ9;
AC Q5LDZ9;
DT 21-JUN-2005, integrated into UniProtKB/TrEMBL.
DT 21-JUN-2005, sequence version 1.
DT 07-FEB-2006, entry version 9.
DE Putative outer membrane protein.
GN OrderedLocusNames=BF1956;
OS Bacteroides fragilis (strain ATCC 25285 / NCTC 9343).
OC Bacteria; Bacteroidetes; Bacteroidetes (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OC NCBI_TaxID=272559;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15746427; DOI=10.1126/science.1107008;
RA Cerdeno-Tarraga A.-M., Patrick S., Crossman L.C., Blakely G.,
RA Abratt V., Lennard N., Poxton I., Duerden B., Harris B., Quail M.A.,
RA Barron A., Clark L., Corton C., Doggett J., Holden M.T.G., Larke N.,
RA Line A., Lord A., Norbertczak H., Ormond D., Price C.,
RA Rabinowitsch E., Woodward J., Barrell B.G., Parkhill J.;
RT "Extensive DNA inversions in the B. fragilis genome control variable
gene expression.";
RL Science 307:1463-1465(2005).
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; CR626927; CAH07654.1; -; Genomic DNA.
DR GO; GO:0019867; C:outer membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
KW Complete proteome; Membrane; Outer membrane; TonB box.
SQ SEQUENCE 1125 AA; 124651 MW; 05A9F2D5D67856C3 CRC64;

Query Match 81.4%; Score 35; DB 2; Length 1125;
Best Local Similarity 66.7%; Pred. No. 2.2e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RVSLSYRF 9
DB 1051 REITLSYRF 1059

RESULT 8
Q93TH9 BACFR PRELIMINARY; PRT; 1125 AA.
ID Q93TH9;
AC Q93TH9;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 1.
DE Outer membrane protein Omp121.
GN OrderedLocusNames=BF1894;
OS Bacteroides fragilis.
OC Bacteria; Bacteroidetes; Bacteroidetes (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OC NCBI_TaxID=817;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC25285;
RX MEDLINE=21856486; PubMed=11867216; DOI=10.1016/S0378-1119(01)00835-6;
RA Wexler H.M., Read E.K., Tomzynski T.J.;
RT "Characterization of omp200, a porin gene complex from Bacteroides
fragilis: omp121 and omp71, gene sequence, deduced amino acid
sequences and predictions of porin structure.";
RL Gene 283:95-105(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=YCH46;
RX PubMed=15466707; DOI=10.1073/pnas.0404172101;
RA Kuwahara T., Yamashita A., Hirakawa H., Nakayama H., Toh H., Okada N.,
RA Kuhara S., Hattori M., Hayaishi T., Ohnishi Y.;

```

```

RT "Genomic analysis of Bacteroides fragilis reveals extensive DNA
RT inversions regulating cell surface adaptation.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:14919-14924(2004).
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AF357210; AAK38604.1; -; Genomic DNA.
DR EMBL; AP006841; BAD48642.1; -; Genomic DNA.
DR GO; GO:0019867; C:outer membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR012910; Plug.
DR InterPro; IPR000531; TonB_dep_rcpt.
DR Pfam; PF07715; Plug; 1.
DR Pfam; PF00593; TonB_dep_Rec; 1.
KW Complete proteome; Membrane; Outer membrane; TonB box.
SQ SEQUENCE 1125 AA; 124651 MW; 05A9F2D5D67856C3 CRC64;

Query Match 81.4%; Score 35; DB 2; Length 1125;
Best Local Similarity 66.7%; Pred. No. 2.2e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RSVLSYRF 9
|:|:|:|:|
Db 1051 REITLSYRF 1059

RESULT 9
ID Q3G2T8_9DELTA PRELIMINARY; PRT; 333 AA.
AC Q3G2T8_
DT 08-NOV-2005, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 1.
DE Hypothetical protein precursor.
GN ORFNames=ProBRAFT_1321.
OS Pelobacter propionicus DSM 2379.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
OC Pelobacteraceae; Pelobacter.
OX NCBI_TaxID=338966;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DSM 2379;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RT "Sequencing of the draft genome and assembly of Pelobacter propionicus
RT DSM 2379.";
RL Submitted (AUG-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DSM 2379;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RA "Annotation of the draft genome assembly of Pelobacter propionicus DSM
RT 2379.";
RL Submitted (AUG-2005) to the EMBL/GenBank/DBJ databases.
CC !- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AAJH01000010; EAO36301.1; -; Genomic DNA.
KW Hypothetical protein; Signal.
FT SIGNAL 1 37
SQ SEQUENCE 333 AA; 37659 MW; B90D457D78EAE109 CRC64;

Query Match 79.1%; Score 34; DB 2; Length 333;
Best Local Similarity 87.5%; Pred. No. 96;

```

```

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 SVLSYRF 9
|:|:|:|:|
Db 326 SVSLEYRF 333

RESULT 10
ID Q6D6D4_ERWCT PRELIMINARY; PRT; 366 AA.
AC Q6D6D4_
DT 16-AUG-2004, integrated into UniProtKB/TrEMBL.
DT 16-AUG-2004, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Outer-membrane protein A.
GN Name=ompA; OrderedLocNames=ECAL751;
OS Erwinia carotovora subsp. atroseptica (Pectobacterium atrosepticum).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Pectobacterium.
OX NCBI_TaxID=29471;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=SCRI 1043 /-ATCC BAA-672;
RX PubMed=15263089; DOI=10.1073/pnas.0402424101;
RA Bell K.S., Sebaihia M., Pritchard L., Holden M.T.G., Hyman L.J.,
RA Holvea M.C., Thomson N.R., Bentley S.D., Churcher L.J.C., Mungall K.,
RA Atkin R., Bason N., Brooks K., Chillingworth T., Clark K., Doggett J.,
RA Fraser A., Hance Z., Hauser H., Jagels K., Moule S., Norbertczak H.,
RA Ormond D., Price C., Quail M.A., Sanders M., Walker D., Whitehead S.,
RA Salmond G.P.C., Birch P.R.J., Parkhill J., Toth I.K.;
RT "Genome sequence of the enterobacterial phytopathogen Erwinia
RT carotovora subsp. atroseptica and characterization of virulence
RT factors.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:11105-11110(2004).
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; BX950851; CAG74656.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0009279; C:outer membrane (sensu Gram-negative Bacteria); IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR006664; Bac_OmpA.
DR InterPro; IPR002368; OmpA.
DR InterPro; IPR006665; OmpA/MotB.
DR InterPro; IPR006690; OMPA_LIKE.
DR InterPro; IPR000498; OmpA_TM.
DR Pfam; PF00691; OmpA; 1.
DR PRINTS; PR01389; OmpA membrane; 1.
DR PRINTS; PR01021; OMPADOMAIN.
DR PRODOM; PD000930; OmpA/MotB; 1.
DR PROSITE; PS01068; OMPA_1; 1.
KW Complete proteome.
SQ SEQUENCE 366 AA; 39013 MW; 7BD65E03C6179F25 CRC64;

Query Match 79.1%; Score 34; DB 2; Length 366;
Best Local Similarity 87.5%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 SVLSYRF 9
|:|:|:|:|
Db 201 SVGLSYRF 208

RESULT 11
ID Q9RM69_ERWCA PRELIMINARY; PRT; 367 AA.
AC Q9RM69_
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 07-FEB-2006, entry version 20.
DE Putative outer-membrane protein A precursor.

```


GN NameompA;
OS Erwinia carotovora.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Pectobacterium.
OX NCBI_TaxID=554;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=MFC10;
RA El-hamel C., Chevalier S., De E., Orange N., Molle G.;
RT "Isolation and characterization of the major outer membrane protein of
RT Erwinia carotovora MFC10";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL; AJ249340; CAB57308.1; -; Genomic_DNA.
DR HSSP; P02934; IQJP.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0002729; C:outer membrane (sensu Gram-negative Bacteria); IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR006664; Bac_OmpA.
DR InterPro; IPR002368; OmpA.
DR InterPro; IPR006665; OmpA/MotB.
DR InterPro; IPR000498; OmpA_TM.
DR Pfam; PF00651; OmpA; 1.
DR Pfam; PF01389; OmpA membrane; 1.
DR PRINTS; PR01021; OMPADOMAIN.
DR PRINTS; PR01022; OUTRMWBRANE.
DR ProDom; PD000930; OmpA/MotB; 1.
KW Signal.
FT SIGNAL.
FT CHAIN 1 21 Potential.
FT CHAIN 22 367 putative outer-membrane protein A.
SQ SEQUENCE 367 AA; 32923 MW; 04F74B421F3DEFB7 CRC64;
Query Match 79.1%; Score 34; DB 2; Length 367;
Best Local Similarity 87.5%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 2 SVLSLYRF 9
DB 196 SVGLSYRF 203
RESULT 12
Q4BPU4 BURVI PRELIMINARY; PRT; 372 AA.
AC Q4BPU4;
DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 13-SEP-2005, sequence version 1.
DT 07-FEB-2006, entry version 2.
DE Hypothetical protein.
GN ORFNames=Bcep1808DRAFT_6246;
OS Burkholderia vietnamiensis G4.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.
OX NCBI_TaxID=269482;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=G4;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RA "Sequencing of the draft genome and assembly of Burkholderia
RT vietnamiensis G4";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=G4;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RA "Annotation of the draft genome assembly of Burkholderia vietnamiensis
RT G4";

RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=G4;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RA Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL; AA0200006; EAM31978.1; -; Genomic_DNA.
DR Hypothetical protein.
KW Hypothetical protein.
SQ SEQUENCE 372 AA; 42840 MW; 2254A94030D5D138 CRC64;
Query Match 79.1%; Score 34; DB 2; Length 372;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
OY 1 RSVLSLYRF 9
DB 68 RATSISYRF 76
RESULT 13
P96773 HAEDU PRELIMINARY; PRT; 403 AA.
ID P96773; Q7BY82;
AC P96773; Q7BY82;
DT 01-MAY-1997, integrated into UniProtKB/TrEMBL.
DT 01-MAY-1997, sequence version 1.
DT 07-FEB-2006, entry version 28.
DE Major outer membrane protein.
GN Name=ompA; Synonyms=omp; OrderedLocusNames=HD0045; ORFNames=HD_0045;
OS Haemophilus ducreyi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=730;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=35000;
RX MEDLINE=97197543; PubMed=9045839;
RA Klesney-Tait J., Hiltke T.J., Maciver I., Spinola S.M., Radolf J.D.,
RA Hansen E.J.;
RT "The major outer membrane protein of Haemophilus ducreyi consists of
RT two ompA homologs";
RL J. Bacteriol. 179:1764-1773 (1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=35000;
RA Klesney-Tait J.A., Hiltke T., Spinola S., Ralldolf J., Hansen E.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=35000HP / ATCC 700724;
RA Munson R.S. Jr., Ray W.C., Mahairas G., Sabo P., Mungur R.,
RA Johnson L., Nguyen D., Wang J., Forst C., Hood L.;
RA "The complete genome sequence of Haemophilus ducreyi";
RT Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL; U60646; AAB49273.1; -; Genomic_DNA.
DR EMBL; A5017143; AAP95060.1; -; Genomic_DNA.
DR HSSP; P02934; IG90.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0009279; C:outer membrane (sensu Gram-negative Bacteria); IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR006664; Bac_OmpA.

```
DR InterPro; IPR002368; OmpA.
DR InterPro; IPR006665; OmpA/MotB.
DR InterPro; IPR000498; OmpA_TM.
DR Pfam; PF00691; OmpA; 1.
DR Pfam; PF01389; OmpA membrane; 1.
DR PRINTS; PRO1021; OMPADOMAIN.
DR PRINTS; PRO1022; OUTRMEMBRANE.
DR ProDom; PD000930; OmpA/MotB; 1.
KW Complete proteome.
SQ SEQUENCE 403 AA; 44172 MW; 44292568EB37736C CRC64;

Query Match 79.1%; Score 34; DB 2; Length 403;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SVSLSYRF 9
Db 247 SVGLSYRF 254

RESULT 14
ID Q2S253_9SPHI PRELIMINARY; PRT; 433 AA.
AC Q2S253;
DT 24-JAN-2006, integrated into UniProtKB/TrEMBL.
DT 24-JAN-2006, sequence version 1.
DT 07-MAR-2006, entry version 3.
DE DnaJ domain protein.
GN ORFNames=SRU_1607;
OS Salinibacter ruber DSM 13855.
OC Bacteria; Bacteroidetes; Sphingobacteriales;
OC Crenotrichaceae; Salinibacter.
OX NCBI_TaxID=309807;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DSM 13855;
RX PubMed=16330755; DOI=10.1073/pnas.0509073102;
RA Mongodin E.F., Nelson K.E., Daugherty S., Deboy R.T., Wister J.,
RA Khouri H., Weidman J., Walsh D.A., Papke R.T., Sanchez Perez G.,
RA Sharma A.K., Nesbo C.L., Macleod D., Baptiste E., Doolittle W.F.,
RA Charlebois R.L., Legault B., Rodriguez-Valera F.;
RT "The genome of Salinibacter ruber: Convergence and gene exchange among
hyperhalophilic bacteria and archaea."
RL Proc. Natl. Acad. Sci. U.S.A. 102:18147-18152(2005).
CC -!- SUBCELLULAR LOCATION: Membrane-bound. Mitochondrial; inner
membrane (By similarity).
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; CP000159; ABC43940.1; -; Genomic DNA.
KW Chaperrone; Inner membrane; Membrane; Protein transport; Translocation;
KW Transmembrane; Transport.
SQ SEQUENCE 433 AA; 48388 MW; 6B9C151D56CB50E1 CRC64;

Query Match 79.1%; Score 34; DB 2; Length 433;
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSVLSLYR 8
Db 185 RSVLSLYR 192

RESULT 15
ID Q9DQ91_9CLOS PRELIMINARY; PRT; 559 AA.
AC Q9DQ91;
DT 01-MAR-2001, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2001, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE RNA-dependent RNA polymerase (fragment).
OS Pineapple mealybug wilt-associated virus 2.

Viruses; ssRNA positive-strand viruses, no DNA stage; Closteroviridae;
Ampelovirus.
OX NCBI_TaxID=136234;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21064595; PubMed=11125151;
RT "Nucleotide sequence, genome organization and phylogenetic analysis of
RT pineapple mealybug wilt-associated virus-2.";
RT J. Gen. Virol. 82:1-7(2001).
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AF283103; AAG13939.1; -; Genomic DNA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR GO; GO:0019079; P:viral genome replication; IEA.
DR InterPro; IPR001788; RNA_dep_RNAPol2.
DR InterPro; IPR007095; RNA_pol_DS_Ps.
DR InterPro; IPR007094; RNA_pol_PSVir.
DR Pfam; PF00978; RdRP_2; 1.
KW RNA-directed RNA polymerase.
FT NON_TER 1
SQ SEQUENCE 559 AA; 64784 MW; 6736F4972E264DD2 CRC64;

Query Match 79.1%; Score 34; DB 2; Length 559;
Best Local Similarity 87.5%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SVSLSYRF 9
Db 53 SVSLDYRF 60

Search completed: August 10, 2006, 23:09:58
Job time : 150 secs
```

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 10, 2006, 23:01:01 ; Search time 18.5455 Seconds
(without alignments)
46.693 Million cell updates/sec

Title: US-10-825-603-1

Perfect score: 43

Sequence: 1 RVSLSYRF 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 80.*

1: Pir1.*

2: Pir2.*

3: Pir3.*

4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	81.4	468	2 F71422	hypothetical prote
2	32	74.4	219	2 S56899	probable membrane
3	32	74.4	257	2 B64352	hypothetical prote
4	32	74.4	323	2 B72224	conserved hypotet
5	32	74.4	338	2 T43440	hypothetical prote
6	32	74.4	380	2 T29875	hypothetical prote
7	32	74.4	516	2 T00791	purple acid phosph
8	32	74.4	682	2 B70121	hypothetical prote
9	31	72.1	160	2 H88114	protein F53C3.6 [i
10	31	72.1	194	2 A10489	conserved hypotet
11	31	72.1	201	2 E75567	hypothetical prote
12	31	72.1	238	2 I40703	outer membrane pro
13	31	72.1	238	2 I62385	outer membrane pro
14	31	72.1	240	2 I62394	outer membrane pro
15	31	72.1	241	2 I62387	outer membrane pro
16	31	72.1	241	2 I62391	outer membrane pro
17	31	72.1	243	2 I62386	outer membrane pro
18	31	72.1	244	2 I62393	outer membrane pro
19	31	72.1	244	2 I62389	outer membrane pro
20	31	72.1	315	2 E83874	nickel ABC transpo
21	31	72.1	337	2 E95871	probable oxidoredu
22	31	72.1	350	1 MMBEAT	outer membrane pro
23	31	72.1	350	2 A16226	outer membrane pro
24	31	72.1	350	2 S07222	outer membrane pro
25	31	72.1	353	2 AD0175	probable outer mem
26	31	72.1	432	2 B86220	protein F22013.31
27	31	72.1	441	2 T00738	hypothetical prote
28	31	72.1	484	2 A58663	catalase [EC 1.11.
29	31	72.1	544	2 S75388	probable phenylala

30	31	72.1	609	2 B75257	arginyl-tRNA synth
31	31	72.1	789	2 H83354	probable TonB-depe
32	31	72.1	863	2 B71343	probable ribosomal
33	31	72.1	1800	2 A11918	serine/threonine k
34	31	72.1	3131	2 T39553	vacuolar protein s
35	30	69.8	111	2 S06385	hypothetical 13.2K
36	30	69.8	128	2 S76824	transposase slr158
37	30	69.8	214	2 G83488	probable permease
38	30	69.8	238	2 S74231	bidirectional hydr
39	30	69.8	283	2 T48332	hypothetical prote
40	30	69.8	303	2 JS0379	hypothetical 35.5K
41	30	69.8	354	2 H70608	probable succinyl-
42	30	69.8	405	2 D90166	hypothetical prote
43	30	69.8	411	2 F86188	protein T25N20.2 [
44	30	69.8	493	2 E69487	protein translocas
45	30	69.8	518	2 H64775	probable membrane

ALIGNMENTS

RESULT 1

F71422

hypothetical protein - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

A:Variety: Columbia

C:Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 09-Jul-2004

C:Accession: F71422

R:Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dir,

P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzenecker, T.; Pohl, T.M.; Terryn, N.; Gie

avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B.

Nature 391, 485-488, 1998

A:Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenech

erhoff, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; An

C.; Chalwatzis, N.

A:Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis tha

A:Reference number: A71400; MUID:98121113; PMID:9461215

A:Accession: F71422

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-468 <BEV>

A:Cross-references: UNIPROT:O23425; UNIPARC:UPI00000A66FB; GB:297339; NID:G2244901; PID

C:Genetics:

A:Map position: 4COP9-4G3845

Query Match 81.4%; Score 35; DB 2; Length 468;
Best Local Similarity 87.5%; Pred. No. 10;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SVLSYRF 9
DB 174 TVLSYRF 181

RESULT 2

S56899

probable membrane protein YJL118w - Yeast (Saccharomyces cerevisiae)

N:Alternate names: hypothetical protein J0742

C:Species: Saccharomyces cerevisiae

C:Date: 08-Jul-1995 #sequence_revision 08-Sep-1995 #text_change 09-Jul-2004

C:Accession: S56899

R:Cziepluch, C.; Korde, E.; Pujol, A.; Jauniaux, J.C.

submitted to the Protein Sequence Database, September 1995

A:Reference number: S56891

A:Accession: S56899

A:Molecule type: DNA

A:Residues: 1-219 <CZI>

A:Cross-references: UNIPROT:P47022; UNIPARC:UPI000013B5E7; EMBL:Z49394; NID:G1008309; P

C:Genetics:

A:Gene: MIPS:YJL118w

A:Cross-references: SGD:S0003654

A:Map position: 10L

C:Superfamily: Saccharomyces cerevisiae probable membrane protein YJL118w

C;Keywords: transmembrane protein

Query Match 74.4%; Score 32; DB 2; Length 219;
Best Local Similarity 77.8%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RSVSLSYRF 9
| | | | |
Db 58 RSVSTVYRF 66

RESULT 3
B64352
hypothetical protein MJ0418 - Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: B64352
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, A.;
; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
rsion, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.
A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A;Reference number: A64300; MUID:96337999; PMID:8688087
A;Accession: B64352
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-257 <BUL>
A;Cross-references: UNIPROT:Q57861; UNIPARC:UPI000013979E; GB:U67494; GB:L77117; NID:gl5
C;Genetics:
A;Map position: FOR376618-377391
A;Start codon: GTG

Query Match 74.4%; Score 32; DB 2; Length 257;
Best Local Similarity 75.0%; Pred. No. 24;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SVSLSYRF 9
| | | | |
Db 22 SVSLAYKF 29

RESULT 4
B72224
conserved hypothetical protein - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: B72224
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
C.M.

Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: B72224
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-323 <ARN>
A;Cross-references: UNIPROT:Q9X120; UNIPARC:UPI000000C123B; GB:AE001808; GB:AE000512; NID
A;Experimental source: strain MSB8
C;Genetics:
A;Gene: TM1660

Query Match 74.4%; Score 32; DB 2; Length 323;
Best Local Similarity 66.7%; Pred. No. 31;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RSVSLSYRF 9
| | | | |
Db 262 KSVSAAYRF 270

RESULT 5

T43440
hypothetical protein DKFZp434K0514.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C;Accession: T43440
R;Koehrer, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, December 1999
A;Reference number: Z22514
A;Accession: T43440
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-338 <AAA>
A;Cross-references: UNIPROT:Q8TBZ3; UNIPARC:UPI000016AC8F; EMBL:AL133558
A;Experimental source: adult testis; clone DKFZp434K0514
C;Genetics:
A;Note: DKFZp434K0514.1

Query Match 74.4%; Score 32; DB 2; Length 338;
Best Local Similarity 65.7%; Pred. No. 32;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RSVSLSYRF 9
| | | | |
Db 130 RPSVSTVYRF 138

RESULT 6
T29875
hypothetical protein F32B5.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Dec-2004
C;Accession: T29875
R;Ledwith, J.; Graves, T.; Biewald, T.
submitted to the EMBL Data Library, May 1997
A;Description: The sequence of C. elegans cosmid F32B5.
A;Reference number: Z20702
A;Accession: T29875
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-380 <LED>
A;Cross-references: UNIPROT:O01853; UNIPARC:UPI000000783FE; EMBL:AF003148; PIDN:AABS4207.
A;Experimental source: strain Bristol N2; clone F32B5
C;Genetics:
A;Gene: CESP:F32B5.2
A;Map position: 1
A;Introns: 47/3; 99/2; 195/3; 227/1; 264/2; 333/3

Query Match 74.4%; Score 32; DB 2; Length 380;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SVSLSYR 8
| | | | |
Db 287 SVSLSYR 293

RESULT 7
T00791
purple acid phosphatase-related protein At2g32770 [similarity] - Arabidopsis thaliana
N;Alternate names: hypothetical protein F24L7.9
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 05-Oct-2004
C;Accession: T00791; C84737
R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul
submitted to the EMBL Data Library, February 1998
A;Description: Arabidopsis thaliana chromosome II BAC F24L7 genomic sequence.
A;Reference number: Z14204
A;Accession: T00791
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-516 <ROU>
A;Cross-references: UNIPROT:O48840; UNIPARC:UPI00000485E3; EMBL:AC003974; NID:g2914688;
A;Experimental source: cultivar Columbia

R.; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.; euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: C84737
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-516 <STO>
A:Cross-references: UNIPARC:UPI00000485E3; GB:AE002093; NID:g2914696; PIDN:AAC04486.1; G
C:Genetics:
A:Gene: At2g32770; F24L7.9
A:Map position: 2
A:Introns: 90/1; 279/2; 324/1; 387/3; 478/3
C:Superfamily: Purple acid phosphatase, kidney bean type; phosphoesterase core homology

Query Match 74.4%; Score 32; DB 2; Length 516;
Best Local Similarity 87.5%; Pred. No. 51;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 SVLSYRF 9
|||||
DB 73 SVLSYSF 80

RESULT 8
B70121
hypothetical protein B80170 - Lyme disease spirochete
C:Species: *Borrelia burgdorferi* (Lyme disease spirochete)
C:Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
C:Accession: B70121
R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White
son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,
Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A:Authors: Smith, H.O.; Venter, J.C.
A:Title: Genomic sequence of a Lyme disease spirochete, *Borrelia burgdorferi*.
A:Reference number: A70100; MUID:98065943; PMID:9403685
A:Accession: B70121
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-682 <KLE>
A:Cross-references: UNIPROT:O51192; UNIPARC:UPI0000057395; GB:AE001128; GB:AE000783; NID
A:Experimental source: strain B31
C:Superfamily: *Borrelia burgdorferi* hypothetical protein B80170

Query Match 74.4%; Score 32; DB 2; Length 682;
Best Local Similarity 85.7%; Pred. No. 69;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 VLSYRF 9
|||||
DB 576 VLSYRF 582

RESULT 9
H88114
protein F53C3.6 [imported] - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C:Accession: H88114
R:Anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode *C. elegans*: a platform for investigating biolog
A:Reference number: A75000; MUID:99069613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_ele
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A:Accession: H88114
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-160 <STO>
A:Cross-references: UNIPARC:UPI000017A590; GB:chr_II; PIDN:AC67457.1; PID:g3786484; GSPD

C:Genetics:
A:Gene: F53C3.6
A:Map position: 2

Query Match 72.1%; Score 31; DB 2; Length 160;
Best Local Similarity 75.0%; Pred. No. 24;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RSVLSYR 8
|||||
DB 4 RQVSISYR 11

RESULT 10

AI0489
conserved hypothetical protein (partial) YPO4026 [imported] - *Yersinia pestis* (strain C
C:Species: *Yersinia pestis*
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 04-Aug-2003
C:Accession: AI0489
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B
deno-farraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A:Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AI0489
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-194 <KUR>
A:Cross-references: UNIPARC:UPI00000CDAD3; GB:AL590842; PIDN:CAC93485.1; PID:g15981930;
C:Genetics:
A:Gene: YPO4026
C:Superfamily: virulence protein, RhuM type

Query Match 72.1%; Score 31; DB 2; Length 194;
Best Local Similarity 85.7%; Pred. No. 30;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 VLSYRF 9
|||||
DB 11 VLSYKF 17

RESULT 11

E75567
hypothetical protein - *Deinococcus radiodurans* (strain R1)
C:Species: *Deinococcus radiodurans*
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: E75567
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; M
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioreistant bacterium *Deinococcus radiodurans* R1.
A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: E75567
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-201 <WHI>
A:Cross-references: UNIPROT:Q9RYB3; UNIPARC:UPI00000C16A8; GB:AE001867; GB:AE000513; N1
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR0037
A:Map position: 1

Query Match 72.1%; Score 31; DB 2; Length 201;
Best Local Similarity 87.5%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RSVLSYR 8
|||||
DB 112 RSPSLSYR 119

RESULT 12

I62385
outer membrane protein A - Citrobacter freundii (fragment)
N:Alternate names: outer membrane protein II
C:Species: Citrobacter freundii
C:Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C:Accession: I62385
R:Lawrence, J.G.; Ochman, H.; Hartl, D.L.
J. Gen. Microbiol. 137, 1911-1921, 1991
A:Title: Molecular and evolutionary relationships among enteric bacteria.
A:Reference number: I62385; PMID:1955870
A:Accession: I62385
C:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-238 <RES>
A:Cross-references: UNIPROT:P24016; UNIPARC:UPI0000130CBF; GB:M63354; NID:g144441; PIDN:
C:Genetics:
A:Gene: ompA
C:Superfamily: outer membrane protein A
C:Keywords: membrane protein
F:99-109/Region: alanine/proline-rich

Query Match 72.1%; Score 31; DB 2; Length 238;
Best Local Similarity 75.0%; Pred. No. 37;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 SVLSYRF 9
DB 85 SVGSYRF 92

RESULT 13

I62385
outer membrane protein ompA - Escherichia vulneris (fragment)
N:Alternate names: outer membrane protein II
C:Species: Escherichia vulneris
C:Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 09-Jul-2004
C:Accession: I62385
R:Lawrence, J.G.; Ochman, H.; Hartl, D.L.
J. Gen. Microbiol. 137, 1911-1921, 1991
A:Title: Molecular and evolutionary relationships among enteric bacteria.
A:Reference number: I62385; PMID:1955870
A:Accession: I62385
C:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-238 <RES>
A:Cross-references: UNIPROT:Q99114; UNIPARC:UPI00000B0580; GB:M63348; NID:g146984; PIDN:
C:Genetics:
A:Gene: ompA
C:Superfamily: outer membrane protein A
C:Keywords: membrane protein
F:98-109/Region: alanine/proline-rich

Query Match 72.1%; Score 31; DB 2; Length 238;
Best Local Similarity 75.0%; Pred. No. 37;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 SVLSYRF 9
DB 85 SVGSYRF 92

RESULT 14

I62394
outer membrane protein ompA - Escherichia blattae (ATCC 33430) (fragment)
N:Alternate names: outer membrane protein II
C:Species: Escherichia blattae
A:Variety: ATCC 33430
C:Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 09-Jul-2004
C:Accession: I62394
R:Lawrence, J.G.; Ochman, H.; Hartl, D.L.
J. Gen. Microbiol. 137, 1911-1921, 1991

A:Title: Molecular and evolutionary relationships among enteric bacteria.
A:Reference number: I40701; PMID:92065252; PMID:1955870
A:Accession: I62394
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-240 <RES>
A:Cross-references: UNIPROT:Q99124; UNIPARC:UPI000016EC3C; GB:M63345; NID:g147002; PIDN:
A:Experimental source: ATCC 33430
C:Genetics:
A:Gene: ompA
C:Superfamily: outer membrane protein A
C:Keywords: membrane protein
F:100-111/Region: alanine/proline-rich

Query Match 72.1%; Score 31; DB 2; Length 240;
Best Local Similarity 75.0%; Pred. No. 37;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 SVLSYRF 9
DB 88 SVGSYRF 95

RESULT 15

I62387
outer membrane protein A - Escherichia blattae (fragment)
N:Alternate names: outer membrane protein II
C:Species: Escherichia blattae
C:Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 09-Jul-2004
C:Accession: I62387
R:Lawrence, J.G.; Ochman, H.; Hartl, D.L.
J. Gen. Microbiol. 137, 1911-1921, 1991
A:Title: Molecular and evolutionary relationships among enteric bacteria.
A:Reference number: I40701; PMID:92065252; PMID:1955870
A:Accession: I62387
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-241 <RES>
A:Cross-references: UNIPROT:Q99124; UNIPARC:UPI0000130CF2; GB:M63343; NID:g146988; PIDN:
C:Genetics:
A:Gene: ompA
C:Superfamily: outer membrane protein A
C:Keywords: membrane protein
F:101-112/Region: alanine/proline-rich

Query Match 72.1%; Score 31; DB 2; Length 241;
Best Local Similarity 75.0%; Pred. No. 38;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 SVLSYRF 9
DB 88 SVGSYRF 95

Search completed: August 10, 2006, 23:11:09
Job time : 18.5455 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

QM protein - protein search, using sw model

Run on: August 10, 2006, 22:52:41 ; Search time 120.273 Seconds
(without alignments)
34.213 Million cell updates/sec

Title: US-10-825-603-2

Perfect score: 33

Sequence: 1 RXVSLSYRX 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_8.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*
- 9: Geneseqp2005s.*
- 10: Geneseqp2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	100.0	9	ADU18130	ADU18130 Immune ce
2	33	100.0	9	ADU18134	ADU18134 Immune ce
3	32	97.0	9	ADU18131	ADU18131 Immune ce
4	30	90.9	68	ADT88429	ADT88429 Variant N
5	30	90.9	336	ABM92272	ABM92272 M. xanthu
6	30	90.9	863	ABU48540	ABU48540 Protein e
7	29	87.9	8	AAY34090	AAY34090 CXCR4 ant
8	29	87.9	8	AAY67591	AAY67591 SDF-1 N-t
9	29	87.9	9	AAY34089	AAY34089 CXCR4 ant
10	29	87.9	9	AAY67590	AAY67590 SDF-1 N-t
11	29	87.9	9	AAY67592	AAY67592 SDF-1 pep
12	29	87.9	9	AAM48662	AAM48662 CXCR4 pep
13	29	87.9	17	AAM48661	AAM48661 CXCR4 pep
14	29	87.9	17	AAM48664	AAM48664 CXCR4 pep
15	29	87.9	18	AAM48663	AAM48663 CXCR4 pep
16	29	87.9	27	ADY76510	ADY76510 Stromal c
17	29	87.9	27	ADY76141	ADY76141 Stromal c
18	29	87.9	27	ADY76132	ADY76132 Stromal c
19	29	87.9	27	ADY76519	ADY76519 Stromal c
20	29	87.9	27	ADY76537	ADY76537 Stromal c
21	29	87.9	27	ADY76411	ADY76411 SDF-1:MI
22	29	87.9	27	ADY76420	ADY76420 SDF-1:MI
23	29	87.9	27	ADY76123	ADY76123 Stromal c

24	29	87.9	27	9	ADY76438	ADY76438 SDF-1:MI
25	29	87.9	27	9	ADY76114	ADY76114 Stromal c
26	29	87.9	27	9	ADY76429	ADY76429 SDF-1:MI
27	29	87.9	27	9	ADY76528	ADY76528 Stromal c
28	29	87.9	28	5	AAM48673	AAM48673 CXCR4 pep
29	29	87.9	29	9	ADY76213	ADY76213 SDF-1:MI
30	29	87.9	29	9	ADY76807	ADY76807 SDF-1:MI
31	29	87.9	29	9	ADY76726	ADY76726 SDF-1:MI
32	29	87.9	29	9	ADY76240	ADY76240 SDF-1:MI
33	29	87.9	29	9	ADY76834	ADY76834 SDF-1:MI
34	29	87.9	29	9	ADY76609	ADY76609 SDF-1:MI
35	29	87.9	29	9	ADY76636	ADY76636 SDF-1:MI
36	29	87.9	29	9	ADY76231	ADY76231 SDF-1:MI
37	29	87.9	29	9	ADY76618	ADY76618 SDF-1:MI
38	29	87.9	29	9	ADY76708	ADY76708 SDF-1:MI
39	29	87.9	29	9	ADY76816	ADY76816 SDF-1:MI
40	29	87.9	29	9	ADY76267	ADY76267 SDF-1:MI
41	29	87.9	29	9	ADY76735	ADY76735 SDF-1:MI
42	29	87.9	29	9	ADY76222	ADY76222 SDF-1:MI
43	29	87.9	29	9	ADY76258	ADY76258 SDF-1:MI
44	29	87.9	29	9	ADY76627	ADY76627 SDF-1:MI
45	29	87.9	29	9	ADY76717	ADY76717 SDF-1:MI

ALIGNMENTS

RESULT 1

ADU18130

ID ADU18130 standard; peptide; 9 AA.

AC ADU18130;

DT 27-JAN-2005 (first entry)

DE Immune cell potentiating factor peptide #1.

KW immunostimulant; cytostatic; antimicrobial; antibacterial; virucide;
KW antiparasitic; antitubercular; tuberculostatic; immune modulation;
KW bacterial infection; viral infection; parasitic infection; cancer;
KW neoplasia; bioterrorism; surgery; post-operative infection;
KW vaccine adjuvant; immune cell potentiating factor.

OS Capra hircus.

OS Synthetic.

EH Key Location/Qualifiers

FT Modified-site 2 /note= "conjugated to fatty acid on the side chain"

FT Modified-site 9

FT /note= "conjugated to fatty acid groups on the side chain and the C-terminus"

FT FT

FT FT

XX XX

PN PN

XX XX

PD PD

XX XX

PF PF

XX XX

PR PR

XX XX

PA PA

XX XX

PI PI

XX XX

DR DR

XX XX

PT PT

XX XX

PT PT

XX XX

XX XX

XX XX

New isolated peptides having an amino terminus and a carboxy terminus useful for the treatment or prevention of viral and bacterial infections, comprise amino acids as given in the specification.

Claim 14; SEQ ID NO 1; 55pp; English.

CC The invention relates to an isolated peptide having an amino terminus and
 CC a carboxy terminus, selected from four amino acid sequences (A1), (A2),
 CC (A3) and (A4), respectively, (A1; ADU18132), (A2; ADU18131), (A3;
 CC ADU18134) and H2N-Arg-Ser(-O-R1)-Val-Ser-Leu-Ser-Tyr-Arg(-H2N-Phe-O-CH2(-
 CC CH(-CH2-O-R3)-O-R2))-Phe-O-CH2(-CH(-CH2-O-R3)-O-R2) (A4; ADU18130),
 CC respectively where R1-R3 are fatty acid groups (preferably stearic acid,
 CC arachidic acid or arachidonic acid). The peptides can be used for the
 CC treatment or prevention of a mammalian disease or disorder such as,
 CC bacterial, viral or parasitic infections and/or cancer or neoplasia, such
 CC as cholera, dysentery, influenza and tuberculosis, as a prophylactic for
 CC short term protection in a bioterrorism area and other contagion environs
 CC and in patients undergoing major surgery to prevent post-operative
 CC infections, as a vaccine adjuvant to provide long-term protection, and
 CC also useful in adjunctive therapy. The peptides act as immune cell
 CC potentiating factors (ICPF) i.e. immune regulators, exhibit a broad
 CC spectrum of therapeutic efficiency and a wide margin of safety to the
 CC host species with respect to toxic and fetal side effects, as associated
 CC with the prior art ICPFs. The peptides are effective in an amount that
 CC produces a serum concentration of greater than 1 microgram/ml, and are
 CC capable of providing an affordable therapy for serious infectious
 CC diseases. This sequence corresponds to a peptide of the invention
 CC isolated from goat serum.
 XX

SQ Sequence 9 AA;

Query Match 100.0%; Score 33; DB 8; Length 9;
 Best Local Similarity 87.5%; Pred. No. 2.1e+06;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RXVSLSYR 8
 | |||||
 DB 1 RSVLSLYR 8

RESULT 2

ADU18134
 ID ADU18134 standard; peptide; 9 AA.

XX

AC ADU18134;

XX 27-JAN-2005 (first entry)

XX Immune cell potentiating factor peptide #5.

DE immunostimulant; cytostatic; antimicrobial; antibacterial; virucide;
 KW antiparasitic; antitubercular; tuberculostatic; immune modulation;
 KW bacterial infection; viral infection; parasitic infection; cancer;
 KW neoplasia; bioterrorism; surgery; post-operative infection;
 KW vaccine adjuvant; immune cell potentiating factor.
 XX

OS Capra hircus.

OS Synthetic.

XX WO2004094455-A2.

XX 04-NOV-2004.

XX 16-APR-2004; 2004WO-US011896.

XX 16-APR-2003; 2003US-0463042P.

XX (GENE-) GENEBACT BIOTECHNOLOGIES INC.

XX Thacker JD, Fuhrer PJ, Willeford KO;

XX WPI; 2004-795526/78.

XX New isolated peptides having an amino terminus and a carboxy terminus
 XX useful for the treatment or prevention of viral and bacterial infections,
 PT comprise amino acids as given in the specification.
 XX

XX Claim 12; SEQ ID NO 5; 55pp; English.

XX

CC The invention relates to an isolated peptide having an amino terminus and
 CC a carboxy terminus, selected from four amino acid sequences (A1), (A2),
 CC (A3) and (A4), respectively, (A1; ADU18132), (A2; ADU18131), (A3;
 CC ADU18134) and H2N-Arg-Ser(-O-R1)-Val-Ser-Leu-Ser-Tyr-Arg(-H2N-Phe-O-CH2(-
 CC CH(-CH2-O-R3)-O-R2))-Phe-O-CH2(-CH(-CH2-O-R3)-O-R2) (A4; ADU18130),
 CC respectively where R1-R3 are fatty acid groups (preferably stearic acid,
 CC arachidic acid or arachidonic acid). The peptides can be used for the
 CC treatment or prevention of a mammalian disease or disorder such as,
 CC bacterial, viral or parasitic infections and/or cancer or neoplasia, such
 CC as cholera, dysentery, influenza and tuberculosis, as a prophylactic for
 CC short term protection in a bioterrorism area and other contagion environs
 CC and in patients undergoing major surgery to prevent post-operative
 CC infections, as a vaccine adjuvant to provide long-term protection, and
 CC also useful in adjunctive therapy. The peptides act as immune cell
 CC potentiating factors (ICPF) i.e. immune regulators, exhibit a broad
 CC spectrum of therapeutic efficiency and a wide margin of safety to the
 CC host species with respect to toxic and fetal side effects, as associated
 CC with the prior art ICPFs. The peptides are effective in an amount that
 CC produces a serum concentration of greater than 1 microgram/ml, and are
 CC capable of providing an affordable therapy for serious infectious
 CC diseases. This sequence corresponds to a peptide of the invention.
 XX

SQ Sequence 9 AA;

Query Match 100.0%; Score 33; DB 8; Length 9;
 Best Local Similarity 87.5%; Pred. No. 2.1e+06;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RXVSLSYR 8
 | |||||
 DB 1 RSVLSLYR 8

RESULT 3

ADU18131
 ID ADU18131 standard; peptide; 9 AA.

XX

AC ADU18131;

XX 27-JAN-2005 (first entry)

XX Immune cell potentiating factor peptide #2.

DE immunostimulant; cytostatic; antimicrobial; antibacterial; virucide;
 KW antiparasitic; antitubercular; tuberculostatic; immune modulation;
 KW bacterial infection; viral infection; parasitic infection; cancer;
 KW neoplasia; bioterrorism; surgery; post-operative infection;
 KW vaccine adjuvant; immune cell potentiating factor.
 XX

OS Capra hircus.

XX WO2004094455-A2.

XX 04-NOV-2004.

XX 16-APR-2004; 2004WO-US011896.

XX 16-APR-2003; 2003US-0463042P.

XX (GENE-) GENEBACT BIOTECHNOLOGIES INC.

XX Thacker JD, Fuhrer PJ, Willeford KO;

XX WPI; 2004-795526/78.

XX New isolated peptides having an amino terminus and a carboxy terminus
 XX useful for the treatment or prevention of viral and bacterial infections,
 PT comprise amino acids as given in the specification.
 XX

XX Claim 8; SEQ ID NO 2; 55pp; English.

XX The invention relates to an isolated peptide having an amino terminus and
 CC a carboxy terminus, selected from four amino acid sequences (A1), (A2),

CC (A3) and (A4), respectively, (A1: ADU18132), (A2: ADU18131), (A3: ADU18134) and H2N-Arg-Ser(-O-R1)-Val-Ser-Leu-Ser-Tyr-Arg(-H2N-Phe-O-CH2(-CH(-CH2-O-R3)-O-R2))Phe-O-CH2(-CH(-CH2-O-R3)-O-R2) (A4: ADU18130), respectively where R1-R3 are fatty acid groups (preferably stearic acid, arachidic acid or arachidonic acid). The peptides can be used for the treatment or prevention of a mammalian disease or disorder such as, bacterial, viral or parasitic infections and/or cancer or neoplasia, such as cholera, dysentery, influenza and tuberculosis, as a prophylactic for short term protection in a bioterrorism area and other contagion environments and in patients undergoing major surgery to prevent post-operative infections, as a vaccine adjuvant to provide long-term protection, and also useful in adjunctive therapy. The peptides act as immune cell potentiating factors (ICPF) i.e. immune regulators, exhibit a broad spectrum of therapeutic efficiency and a wide margin of safety to the host species with respect to toxic and fetal side effects, as associated with the prior art ICPFs. The peptides are effective in an amount that produces a serum concentration of greater than 1 microgram/ml, and are capable of providing an affordable therapy for serious infectious diseases. This sequence corresponds to a peptide of the invention.

XX Sequence 9 AA;

Query Match 97.0%; Score 32; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXVSLSYR 8
| | | | |
DB 1 RXVSLSYR 8

RESULT 4

ADT88429
ID ADT88429 standard; protein; 68 AA.

AC ADT88429;

XX 27-JAN-2005 (first entry)

DE Variant NMeA-2-SDF-lalpa SEQ ID NO:5.

XX chemokine; CXCR4; CCR5; anti-HIV; antiviral; antiasthmatic;
KW neuroprotective; antiarthritic; antirheumatic; antiarteriosclerotic;
KW gene therapy; HIV; stromal cell-derived factor-1; SDF-lalpa; variant.

OS Homo sapiens.
OS Synthetic.

XX Key Location/Qualifiers
FH Modified-site 2 /note= "N-Methyl-Alanine"
FT

XX WO2004094465-A2.

XX 04-NOV-2004.

XX 23-APR-2004; 2004WO-US012708.

XX 23-APR-2003; 2003US-0464714P.

XX (UYIL-) UNIV ILLINOIS OFFICE TECHNICAL MANAGEMENT.

XX Huang Z;

XX WPI; 2004-775906/76.

XX New synthetic polypeptides that mimic chemokine function, useful for
PT diagnosing, preventing or treating chemokine-related disorders or HIV
PT infection.

XX Claim 1; SEQ ID NO 5; 80pp; English.

XX The invention relates to a novel synthetic polypeptide that mimics

CC chemokine function. The polypeptide comprises a sequence selected from
CC any of the 15 sequences of 60-75 amino acids fully defined in the
CC specification (ADT88426-ADT88433 and ADT88435-ADT88441), and a dimer
CC formed between 2 sequences of 75 bp fully defined in the specification
CC (ADT88442 and ADT88443, or ADT88444 and ADT88445). The polypeptide is an
CC antagonist or an agonist of CXCR4 or CCR5. The antagonist of CXCR4
CC comprises a sequence of 68-71 amino acids fully defined in the
CC specification (ADT88427-ADT88433 or ADT88436). The antagonist of CCR5
CC comprises a sequence of 61 or 71 amino acids fully defined in the
CC specification (ADT88435 and ADT88436, respectively). The agonist of CCR5
CC comprises a sequence of 71 amino acids fully defined in the specification
CC (ADT88440), and the agonist of CXCR4 also comprises a sequence of 71
CC amino acids fully defined in the specification (ADT88439). Alternatively,
CC the polypeptide comprises at least one D-amino acid and/or N-methylated,
CC amino acid of an amino acid sequence having at least 75, 85, 90 or 95%
CC sequence identity with any of the above-mentioned amino acid sequences.
CC The polypeptide may also comprise a sequence modified to have at least
CC one D-amino acid or at least one N-methylated amino acid comprising any
CC of the above-mentioned amino acid sequences. The polypeptide comprises a
CC label selected from fluorescent, radio and enzymatic label. A polypeptide
CC of the invention has anti-HIV, antiviral, antiasthmatic, neuroprotective,
CC antiarthritic, antirheumatic, and antiarteriosclerotic activity, and may
CC have a use in gene therapy. The composition and methods are useful for
CC diagnosing, preventing or treating chemokine-related disorders or HIV
CC infection. The present sequence represents a variant of the human stromal
CC cell-derived factor-1 (SDF-lalpa) protein, where amino acid 2 of the
CC wild-type sequence (ADT88425) has been methylated.

XX SQ Sequence 68 AA;

Query Match 90.9%; Score 30; DB 8; Length 68;

Best Local Similarity 75.0%; Pred. No. 74;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RXVSLSYR 8
: | | | | |

DB 1 KAVSLSYR 8

RESULT 5

ABM92272

ID ABM92272 standard; protein; 336 AA.

AC ABM92272;

XX 02-JUN-2005 (first entry)

XX M. xanthus protein sequence, seq id 11471.

XX Transgenic plant; DNA replication; gene regulation; gene expression.

OS Myxococcus xanthus.

PN US6833447-B1.

XX 21-DEC-2004.

XX 10-JUL-2001; 2001US-00902540.

XX 10-JUL-2000; 2000US-0217883P.

XX (MONS) MONSANTO TECHNOLOGY LLC.

XX Goldman BS, Hinkle GJ, Slater SC, Wiegand RC;

XX WPI; 2005-028716/03.

XX New substantially purified Myxococcus xanthus nucleic acid molecule
PT encoding a nitrite reductase, useful for determining gene expression,
PT identifying mutations in a gene of interest, and for constructing
PT mutations in a gene of interest.

XX Example 2; SEQ ID NO 11471; 25pp; English.

XX The invention relates to a substantially purified nucleic acid molecule
 CC encoding a nitrite reductase of SEQ ID NO. 11926. Further disclosed is a
 CC recombinant DNA construct for expression of a nitrite reductase gene in a
 CC plant cell, and a plant cell comprising the recombinant DNA construct.
 CC The nucleic acid is useful for determining gene expression, identifying
 CC mutations in a gene of interest, and for constructing mutations in a gene
 CC of interest. Sequences given in records for SEQ IDs 9692-16825 represent
 CC a group of 7134 *Mycobacterium xanthus* proteins and peptides. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from USPTO
 XX
 XX Sequence 336 AA;

Query Match 90.9%; Score 30; DB 9; Length 336;
 Best Local Similarity 75.0%; Pred. No. 4e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RXVSLSYR 8
 | : : : :
 Db 35 RAVSLNYR 42

RESULT 6
 ABU48540
 ID ABU48540 standard; protein; 863 AA.

XX AC ABU48540;

DT 19-JUN-2003 (first entry)

DE Protein encoded by Prokaryotic essential gene #34067.

XX Antisense; prokaryotic essential gene; cell proliferation; drug design.

OS *Treponema pallidum*.

XX WO200277183-A2.

XX 03-OCT-2002.

XX 21-MAR-2002; 2002WO-US009107.

XX 21-MAR-2001; 2001US-00815242.

XX 06-SEP-2001; 2001US-00948993.

XX 25-OCT-2001; 2001US-0342923P.

XX 08-FEB-2002; 2002US-00072851.

XX 06-MAR-2002; 2002US-0362699P.

XX (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

XX Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX WPI; 2003-029926/02.

XX N-PSDB; ACA52410.

XX New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.

XX Claim 25; SEQ ID NO 76464; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for

CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 863 AA;

Query Match 90.9%; Score 30; DB 6; Length 863;
 Best Local Similarity 75.0%; Pred. No. 1.1e+03;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RXVSLSYR 8
 | : : : :
 Db 135 RTVALSYR 142

RESULT 7
 AAY34090

ID AAY34090 standard; protein; 8 AA.

XX AC AAY34090;

DT 29-NOV-1999 (first entry)

XX CXCR4 antagonist SDF-1 peptide analogue.

XX CXC chemokine receptor 4; CXCR4; antagonist; medicament; T-cell;
 XX interferon gamma; autoimmune disease; multiple sclerosis; cancer;
 XX angiogenesis; stromal cell derived factor 1; SDF-1.

XX Synthetic.

XX Key Location/Qualifiers

XX Cross-links 8

XX /note= "a lysine residue or a bridge-forming moiety
 XX covalently links this peptide to another peptide of the
 XX same sequence (kgvs1src)"

XX WO9947158-A2.

XX 23-SEP-1999.

XX 12-MAR-1999; 99WO-CA000221.

XX 13-MAR-1998; 98CA-02226391.

XX 14-AUG-1998; 98CA-02245224.

XX (UYBR-) UNIV BRITISH COLUMBIA.

XX Clark-Lewis I, Gong J, Duronio V;

XX WPI; 1999-561857/47.

XX Use of CXC chemokine receptor 4 for treating autoimmune disease and
 PT cancer.

PS Disclosure; Fig 14; 71pp; English.

CC The invention relates to the use of a CXCR4 chemokine receptor 4 (CXCR4) antagonist for the manufacture of a medicament for reducing interferon gamma production by T-cells in a mammal. The CXCR4 antagonist can be used to treat or to design a medicament to treat, an autoimmune disease, multiple sclerosis, cancer, or for inhibiting angiogenesis. The CXCR4 antagonists may be peptide compounds comprising a substantially purified peptide fragment, analogue or a pharmacologically acceptable salt of stromal cell derived factor 1 (SDF-1). The present sequence represents the N-terminal fragment of a SDF-1 protein analogue. This fragment can be used as the CXCR4 antagonist

XX
SQ Sequence 8 AA;

Query Match 87.9%; Score 29; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 2.1e+06;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RXVLSYSR 8
: |||||
Db 1 KGVLSYSR 8

RESULT 8

AAV67591
ID AAY67591 standard; peptide; 8 AA.

XX
AC AAY67591;

XX
DT 13-JUN-2000 (first entry)

XX
DE SDF-1 N-terminal peptide as CXCR4 antagonist.

XX
KW SDF-1; CXCR4; CXCR4 chemokine receptor 4; gamma-interferon; cancer; gout; autoimmune disease; multiple sclerosis; rheumatoid arthritis; psoriasis; type 1 diabetes; ulcerative colitis; lupus; antagonist; antitumor; stromal cell derived factor one; anti-inflammatory; immunomodulatory.

XX
OS Unidentified.

XX
PN WO200009152-A1.

XX
PD 24-FEB-2000.

XX
PF 16-AUG-1999; 99WO-CA000750.

XX
PR 14-AUG-1998; 98CA-02245224.

XX
PA (UYBR-) UNIV BRITISH COLUMBIA.

XX
PI Clark-Lewis I, Gong J, Duronio V, Salari H;

XX
DR WPI; 2000-224175/19.

XX
PT Therapeutic composition containing CXCR4 antagonist, useful for treating autoimmune disease, especially multiple sclerosis and cancer.

XX
PS Claim 19; Page 54; 86pp; English.

XX The invention provides a therapeutic composition containing an antagonist of CXCR4 (CXCR4 chemokine receptor 4) and an excipient. The compositions are specifically used to reduce production of gamma-interferon by T cells, particularly for treating autoimmune disease, especially multiple sclerosis but also e.g. Guillain-Barre syndrome, amyotrophic lateral sclerosis, rheumatoid arthritis, psoriasis, type 1 diabetes, ulcerative colitis, gout, lupus and transplant rejection; to treat cancer by inhibiting angiogenesis; inhibition of restenosis; and when labeled, to evaluate in vivo pharmacokinetics, or to determine disease progression and susceptibility, or as targeting agents for delivery of other therapeutic agents. The antagonist is selected from SDF-1 (stromal cell derived factor one) peptide fragments, SDF-1 being the only known natural ligand for CXCR4. The present sequence represents a SDF-1 peptide that

CC can be used as a CXCR4 antagonist

XX
SQ Sequence 8 AA;

Query Match 87.9%; Score 29; DB 3; Length 8;
Best Local Similarity 75.0%; Pred. No. 2.1e+06;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RXVLSYSR 8
: |||||
Db 1 KGVLSYSR 8

RESULT 9

AAV34089
ID AAY34089 standard; protein; 9 AA.

XX
AC AAY34089;

XX
DT 29-NOV-1999 (first entry)

XX
DE CXCR4 antagonist SDF-1 peptide analogue.

XX
KW CXC chemokine receptor 4; CXCR4; antagonist; medicament; T-cell; interferon gamma; autoimmune disease; multiple sclerosis; cancer; angiogenesis; stromal cell derived factor 1; SDF-1.

XX
OS Synthetic.

XX
FH Key Location/Qualifiers

FT Cross-links

FT /notes= " the Cys residue is covalently linked to another peptide of the same sequence (kgvlsysrc) by a disulphide bond"

XX
PN WO9947158-A2.

XX
PD 23-SEP-1999.

XX
PF 12-MAR-1999; 99WO-CA000221.

XX
PR 13-MAR-1998; 98CA-02226391.

XX
PR 14-AUG-1998; 98CA-02245224.

XX
PA (UYBR-) UNIV BRITISH COLUMBIA.

XX
PI Clark-Lewis I, Gong J, Duronio V;

XX
DR WPI; 1999-561857/47.

XX
PT Use of CXCR4 chemokine receptor 4 for treating autoimmune disease and cancer.

XX
PS Claim 14; Fig 14; 71pp; English.

XX The invention relates to the use of a CXCR4 chemokine receptor 4 (CXCR4) antagonist for the manufacture of a medicament for reducing interferon gamma production by T-cells in a mammal. The CXCR4 antagonist can be used to treat or to design a medicament to treat, an autoimmune disease, multiple sclerosis, cancer, or for inhibiting angiogenesis. The CXCR4 antagonists may be peptide compounds comprising a substantially purified peptide fragment, analogue or a pharmacologically acceptable salt of stromal cell derived factor 1 (SDF-1). The present sequence represents the N-terminal fragment of a SDF-1 protein analogue. This fragment can be used as the CXCR4 antagonist

XX
SQ Sequence 9 AA;

Query Match 87.9%; Score 29; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 2.1e+06;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RXVLSYSR 8

```

Db      : |||||
        1 KGVSLSYR 8

RESULT 10
AAV67590
ID AAY67590 standard; peptide; 9 AA.
XX
AC AAY67590;
XX
DT 13-JUN-2000 (first entry)
XX
DE SDF-1 N-terminal peptide as CXCR4 antagonist.
XX
KW SDF-1; CXCR4; CXC chemokine receptor 4; gamma-interferon; cancer; gout;
KW autoimmune disease; multiple sclerosis; rheumatoid arthritis; psoriasis;
KW type 1 diabetes; ulcerative colitis; lupus; antagonist; antitumour;
KW stromal cell derived factor one; anti-inflammatory; immunomodulatory.
XX
OS Unidentified.
XX
PN WO200009152-A1.
XX
PD 24-FEB-2000.
XX
PF 16-AUG-1999; 99WO-CA000750.
XX
PR 14-AUG-1998; 98CA-02245224.
XX
PA (UYBR-) UNIV BRITISH COLUMBIA.
XX
PI Clark-Lewis I, Gong J, Duronio V, Salari H;
XX
DR WPI; 2000-224175/19.
XX
PT Therapeutic composition containing CXCR4 antagonist, useful for treating
PT autoimmune disease, especially multiple sclerosis and cancer.
XX
PS Claim 14; Page 52; 88pp; English.
XX
CC The invention provides a therapeutic composition containing an antagonist
CC of CXCR4 (CXC chemokine receptor 4) and an excipient. The compositions
CC are specifically used: to reduce production of gamma-interferon by T
CC cells, particularly for treating autoimmune disease, especially multiple
CC sclerosis but also e.g. Guillain-Barre syndrome, amyotrophic lateral
CC sclerosis, rheumatoid arthritis, psoriasis, type 1 diabetes, ulcerative
CC colitis, gout, lupus and transplant rejection; to treat cancer by
CC inhibiting angiogenesis; inhibition of restenosis; and when labeled, to
CC evaluate in vivo pharmacokinetics, or to determine disease progression
CC and susceptibility, or as targeting agents for delivery of other
CC therapeutic agents. The antagonist is selected from SDF-1 (stromal cell
CC derived factor one) peptide fragments, SDF-1 being the only known natural
CC ligand for CXCR4. The present sequence represents a SDF-1 peptide that
CC can be used as a CXCR4 antagonist
XX
SQ Sequence 9 AA;

Query Match      87.9%; Score 29; DB 3; Length 9;
Best Local Similarity 75.0%; Pred. No. 2.1e+06;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy      1 RXVSLSYR 8
        : |||||
Db      1 KGVSLSYR 8

RESULT 12
AAV48662
ID AAM48662 standard; peptide; 9 AA.
XX
AC AAM48662;
XX
DT 20-MAY-2002 (first entry)
XX
DE CXCR4 peptide antagonist SEQ ID NO 14.
XX
KW CRCX4; haematopoietic cell; chemokine receptor-4; cytostatic;
KW immunosuppressive; cancer; autoimmune disease; peripheral blood locus;
KW cell multiplication.
XX
OS Synthetic.
XX
PN WO200185196-A2.
XX

```

```

Db      : |||||
        1 KGVSLSYR 8

RESULT 10
AAV67590
ID AAY67590 standard; peptide; 9 AA.
XX
AC AAY67590;
XX
DT 13-JUN-2000 (first entry)
XX
DE SDF-1 N-terminal peptide as CXCR4 antagonist.
XX
KW SDF-1; CXCR4; CXC chemokine receptor 4; gamma-interferon; cancer; gout;
KW autoimmune disease; multiple sclerosis; rheumatoid arthritis; psoriasis;
KW type 1 diabetes; ulcerative colitis; lupus; antagonist; antitumour;
KW stromal cell derived factor one; anti-inflammatory; immunomodulatory.
XX
OS Unidentified.
XX
PN WO200009152-A1.
XX
PD 24-FEB-2000.
XX
PF 16-AUG-1999; 99WO-CA000750.
XX
PR 14-AUG-1998; 98CA-02245224.
XX
PA (UYBR-) UNIV BRITISH COLUMBIA.
XX
PI Clark-Lewis I, Gong J, Duronio V, Salari H;
XX
DR WPI; 2000-224175/19.
XX
PT Therapeutic composition containing CXCR4 antagonist, useful for treating
PT autoimmune disease, especially multiple sclerosis and cancer.
XX
PS Claim 14; Page 52; 88pp; English.
XX
CC The invention provides a therapeutic composition containing an antagonist
CC of CXCR4 (CXC chemokine receptor 4) and an excipient. The compositions
CC are specifically used: to reduce production of gamma-interferon by T
CC cells, particularly for treating autoimmune disease, especially multiple
CC sclerosis but also e.g. Guillain-Barre syndrome, amyotrophic lateral
CC sclerosis, rheumatoid arthritis, psoriasis, type 1 diabetes, ulcerative
CC colitis, gout, lupus and transplant rejection; to treat cancer by
CC inhibiting angiogenesis; inhibition of restenosis; and when labeled, to
CC evaluate in vivo pharmacokinetics, or to determine disease progression
CC and susceptibility, or as targeting agents for delivery of other
CC therapeutic agents. The antagonist is selected from SDF-1 (stromal cell
CC derived factor one) peptide fragments, SDF-1 being the only known natural
CC ligand for CXCR4. The present sequence represents a SDF-1 peptide that
CC can be used as a CXCR4 antagonist
XX
SQ Sequence 9 AA;

Query Match      87.9%; Score 29; DB 3; Length 9;
Best Local Similarity 75.0%; Pred. No. 2.1e+06;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy      1 RXVSLSYR 8
        : |||||
Db      1 KGVSLSYR 8

RESULT 11
AAV67592
ID AAY67592 standard; peptide; 9 AA.
XX
AC AAY67592;
XX
DT 13-JUN-2000 (first entry)
XX

```

PD 15-NOV-2001.
 XX 09-MAY-2001; 2001WO-CA000659.
 PF
 XX
 XX 09-MAY-2000; 2000CA-02305787.
 PR
 XX 19-MAY-2000; 2000US-0205467P.
 XX
 XX (UYBR-) UNIV BRITISH COLUMBIA.
 PA (CHEM-) CHEMOKINE THERAPEUTICS CORP.
 XX
 XX Tudan CR, Merzouk A, Arab L, Saxena G, Eaves CJ, Cashman J;
 PI Clark-Lewis I, Salari H;
 PI WPI; 2002-106073/14.
 XX
 XX Promoting the rate of hematopoietic cell multiplication for treating a
 PT cancer involves administering chemokine receptor antagonist to the cells.
 XX
 XX Disclosure; Page 17; 68pp; English.
 XX
 XX The invention relates to a method of promoting the rate of hematopoietic
 CC cell multiplication comprising administering chemokine receptor-4 (CXCR4)
 CC antagonist (AAM48656-AAM48701) to hematopoietic cells. The antagonist
 CC has cytostatic and immunosuppressive activity and is useful for treating
 CC cancer or autoimmune disease in a patient; to promote the rate of
 CC hematopoietic cell multiplication; to formulate a medicament for
 CC increasing the circulation of the hematopoietic cells in a patient; for
 CC mobilising hematopoietic cells from a narrow locus to a peripheral blood
 CC locus; in the treatment of hematopoietic cells in vitro and in vivo. The
 CC CXCR4 antagonists stimulates hematopoietic cell multiplication, self-
 CC renewal, expansion and proliferation of peripheralisation in vivo
 XX
 XX Sequence 9 AA;
 SQ
 Query Match 87.9%; Score 29; DB 5; Length 9;
 Best Local Similarity 75.0%; Pred. No. 2.1e+06;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 RXVSLSYR 8
 Db : |||||
 1 KGVLSYSR 8
 RESULT 13
 AAM48661
 ID AAM48661 standard; peptide; 17 AA.
 XX
 AC AAM48661;
 XX
 XX 20-MAY-2002 (first entry)
 DT
 XX CXCR4 peptide antagonist SEQ ID NO 13.
 DE
 XX 'CRCX4; hematopoietic cell; chemokine receptor-4; cytostatic;
 KW immunosuppressive; cancer; autoimmune disease; peripheral blood locus;
 KW cell multiplication.
 XX
 OS Synthetic.
 XX
 XX WO200185196-A2.
 XX
 XX 15-NOV-2001.
 XX
 XX 09-MAY-2001; 2001WO-CA000659.
 XX
 XX 09-MAY-2000; 2000CA-02305787.
 PR
 XX 19-MAY-2000; 2000US-0205467P.
 XX
 XX (UYBR-) UNIV BRITISH COLUMBIA.
 PA (CHEM-) CHEMOKINE THERAPEUTICS CORP.
 XX
 XX Tudan CR, Merzouk A, Arab L, Saxena G, Eaves CJ, Cashman J;
 PI Clark-Lewis I, Salari H;

XX WPI; 2002-106073/14.
 DR
 XX Promoting the rate of hematopoietic cell multiplication for treating a
 PT cancer involves administering chemokine receptor antagonist to the cells.
 XX
 XX Disclosure; Page 17; 68pp; English.
 XX
 XX The invention relates to a method of promoting the rate of hematopoietic
 CC cell multiplication comprising administering chemokine receptor-4 (CXCR4)
 CC antagonist (AAM48656-AAM48701) to hematopoietic cells. The antagonist
 CC has cytostatic and immunosuppressive activity and is useful for treating
 CC cancer or autoimmune disease in a patient; to promote the rate of
 CC hematopoietic cell multiplication; to formulate a medicament for
 CC increasing the circulation of the hematopoietic cells in a patient; for
 CC mobilising hematopoietic cells from a narrow locus to a peripheral blood
 CC locus; in the treatment of hematopoietic cells in vitro and in vivo. The
 CC CXCR4 antagonists stimulates hematopoietic cell multiplication, self-
 CC renewal, expansion and proliferation of peripheralisation in vivo
 XX
 XX Sequence 17 AA;
 SQ
 Query Match 87.9%; Score 29; DB 5; Length 17;
 Best Local Similarity 75.0%; Pred. No. 28;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 RXVSLSYR 8
 Db : |||||
 1 KGVLSYSR 8
 RESULT 14
 AAM48664
 ID AAM48664 standard; peptide; 17 AA.
 XX
 AC AAM48664;
 XX
 XX 20-MAY-2002 (first entry)
 DT
 XX CXCR4 peptide antagonist SEQ ID NO 16.
 DE
 XX 'CRCX4; hematopoietic cell; chemokine receptor-4; cytostatic;
 KW immunosuppressive; cancer; autoimmune disease; peripheral blood locus;
 KW cell multiplication.
 XX
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 10
 FT /note= "X = a linking moiety, X may be an amino acid like
 FT lysine, ornithine or any natural or unnatural amino acid
 FT serving as a linker between each of the arginines at
 FT position 8 in each sequence"
 FT
 XX WO200185196-A2.
 PN
 XX 15-NOV-2001.
 PD
 XX
 XX 09-MAY-2001; 2001WO-CA000659.
 XX
 XX 09-MAY-2000; 2000CA-02305787.
 PR
 XX 19-MAY-2000; 2000US-0205467P.
 XX
 XX (UYBR-) UNIV BRITISH COLUMBIA.
 PA (CHEM-) CHEMOKINE THERAPEUTICS CORP.
 XX
 XX Tudan CR, Merzouk A, Arab L, Saxena G, Eaves CJ, Cashman J;
 PI Clark-Lewis I, Salari H;
 PI WPI; 2002-106073/14.
 DR
 XX Promoting the rate of hematopoietic cell multiplication for treating a
 PT cancer involves administering chemokine receptor antagonist to the cells.

XX Disclosure; Page 17; 68pp; English.

PS The invention relates to a method of promoting the rate of haematopoietic

XX cell multiplication comprising administering chemokine receptor-4 (CXCR4)

CC antagonist (AAM48656-AA48701) to haematopoietic cells. The antagonist

CC has cytostatic and immunosuppressive activity and is useful for treating

CC cancer or autoimmune disease in a patient; to promote the rate of

CC haematopoietic cell multiplication; to formulate a medicament for

CC increasing the circulation of the haematopoietic cells in a patient; for

CC mobilising haematopoietic cells from a narrow locus to a peripheral blood

CC locus; in the treatment of haematopoietic cells in vitro and in vivo. The

CC CXCR4 antagonists stimulates haematopoietic cell multiplication, self-

CC renewal, expansion and proliferation of peripheralisation in vivo. The

CC present sequence shows a dipeptide antagonist construct that can also be

CC applied to SEQ ID NO 28-31 (AAM48669-AA48672)

XX

SQ Sequence 17 AA;

Query Match 87.9%; Score 29; DB 5; Length 17;

Best Local Similarity 75.0%; Pred. No. 28;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RXVSLSYR 8

: |||||

Db 1 KGVSLSYR 8

RESULT 15

AAM48663

ID AAM48663 standard; peptide; 18 AA.

XX

AC AAM48663;

XX

DT 20-MAY-2002 (first entry)

DE CXCR4 peptide antagonist SEQ ID NO 15.

XX

KW CRCX4; haematopoietic cell; chemokine receptor-4; cytostatic;

KW immunosuppressive; cancer; autoimmune disease; peripheral blood locus;

KW cell multiplication.

XX

OS Synthetic.

XX

FH Key

FT Disulfide-bond 9..10

FT /note= "Two 9 amino acid peptides joined by a disulfide

FT bond between each of the cysteines at position 9 in each

FT sequence"

XX

PN WO200185196-A2.

XX

PD 15-NOV-2001.

XX

PF 09-MAY-2001; 2001WO-CA000659.

XX

PR 09-MAY-2000; 2000CA-02305787.

PR 19-MAY-2000; 2000US-0205467P.

XX

PA (UYBR-) UNIV BRITISH COLUMBIA.

PA (CHEM-) CHEMOKINE THERAPEUTICS CORP.

XX

PI Tudan CR, Merzouk A, Arab L, Saxena G, Eaves CJ, Cashman J;

PI Clark-Lewis I, Salari H;

XX

DR WPI; 2002-106073/14.

XX

PT Promoting the rate of hematopoietic cell multiplication for treating a

PT cancer involves administering chemokine receptor antagonist to the cells.

XX

PS Disclosure; Page 17; 68pp; English.

XX

CC The invention relates to a method of promoting the rate of haematopoietic

CC cell multiplication comprising administering chemokine receptor-4 (CXCR4)

CC antagonist (AAM48656-AA48701) to haematopoietic cells. The antagonist

CC has cytostatic and immunosuppressive activity and is useful for treating

CC cancer or autoimmune disease in a patient; to promote the rate of

CC haematopoietic cell multiplication; to formulate a medicament for

CC increasing the circulation of the haematopoietic cells in a patient; for

CC mobilising haematopoietic cells from a narrow locus to a peripheral blood

CC locus; in the treatment of haematopoietic cells in vitro and in vivo. The

CC CXCR4 antagonists stimulates haematopoietic cell multiplication, self-

CC renewal, expansion and proliferation of peripheralisation in vivo. The

CC present sequence shows a dipeptide antagonist construct that can also be

CC applied to SEQ ID NO 28-31 (AAM48669-AA48672)

XX

SQ Sequence 18 AA;

Query Match 87.9%; Score 29; DB 5; Length 18;

Best Local Similarity 75.0%; Pred. No. 30;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RXVSLSYR 8

: |||||

Db 1 KGVSLSYR 8

Search completed: August 10, 2006, 23:00:37

Job time : 122.273 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 10, 2006, 23:11:26 ; Search time 69.0909 Seconds
(without alignments)
40.227 Million cell updates/sec

Title: US-10-825-603-3

Perfect score: 28

Sequence: 1 VLSYSR 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:*

1: /EMC_Celerra_SID33/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /EMC_Celerra_SID33/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
3: /EMC_Celerra_SID33/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
4: /EMC_Celerra_SID33/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
5: /EMC_Celerra_SID33/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
6: /EMC_Celerra_SID33/ptodata/2/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	100.0	6	5	US-10-825-603-3
2	28	100.0	8	3	US-09-852-424-17
3	28	100.0	8	3	US-09-852-424-131
4	28	100.0	8	3	US-09-835-107-11
5	28	100.0	8	3	US-09-835-107-32
6	28	100.0	8	4	US-10-086-177A-11
7	28	100.0	8	4	US-10-086-177A-32
8	28	100.0	8	5	US-10-222-703A-805
9	28	100.0	9	3	US-09-852-424-14
10	28	100.0	9	3	US-09-852-424-15
11	28	100.0	9	3	US-09-852-424-16
12	28	100.0	9	3	US-09-852-424-130
13	28	100.0	9	3	US-09-852-424-132
14	28	100.0	9	3	US-09-835-107-6
15	28	100.0	9	3	US-09-835-107-7
16	28	100.0	9	3	US-09-835-107-9
17	28	100.0	9	3	US-09-835-107-10
18	28	100.0	9	3	US-09-835-107-31
19	28	100.0	9	4	US-10-086-177A-6
20	28	100.0	9	4	US-10-086-177A-7
21	28	100.0	9	4	US-10-086-177A-9
22	28	100.0	9	4	US-10-086-177A-10
23	28	100.0	9	4	US-10-086-177A-31
24	28	100.0	9	5	US-10-825-603-1
25	28	100.0	9	5	US-10-825-603-2
26	28	100.0	9	5	US-10-825-603-5
27	28	100.0	9	5	US-10-222-703A-802

28 100.0 9 5 US-10-945-674A-14 Sequence 14, Appl
29 28 100.0 9 5 US-10-945-674A-15 Sequence 15, Appl
30 28 100.0 9 5 US-10-945-674A-16 Sequence 16, Appl
31 28 100.0 9 5 US-10-945-674A-134 Sequence 134, App
32 28 100.0 9 5 US-10-945-674A-136 Sequence 136, App
33 28 100.0 9 6 US-11-060-031-2 Sequence 2, Appli
34 28 100.0 9 6 US-11-060-031-3 Sequence 3, Appli
35 28 100.0 9 6 US-11-136-097-2 Sequence 2, Appli
36 28 100.0 9 6 US-11-136-097-3 Sequence 3, Appli
37 28 100.0 10 3 US-09-835-107-8 Sequence 8, Appli
38 28 100.0 10 4 US-10-086-177A-8 Sequence 8, Appli
39 28 100.0 10 6 US-11-060-031-4 Sequence 4, Appli
40 28 100.0 10 6 US-11-136-097-4 Sequence 39, Appl
41 28 100.0 11 4 US-10-343-654-39 Sequence 12, Appl
42 28 100.0 11 5 US-10-768-974-12 Sequence 6, Appli
43 28 100.0 14 5 US-10-222-703A-6 Sequence 8, Appli
44 28 100.0 14 5 US-10-222-703A-8 Sequence 818, App
45 28 100.0 14 5 US-10-222-703A-818

ALIGNMENTS

RESULT 1

US-10-825-603-3
; Sequence 3, Application US/10825603
; Publication No. US20050042635A1
; GENERAL INFORMATION:
; APPLICANT: THACKER, JAMES D.
; APPLICANT: FUHRER, PETER J.
; APPLICANT: WILLEFORD, KENNETH O.
; TITLE OF INVENTION: PROPHYLACTIC AND THERAPEUTIC BENEFITS OF A NEW CLASS OF
; TITLE OF INVENTION: IMMUNE STIMULATING PEPTIDES
; FILE REFERENCE: 54442-20005.00
; CURRENT APPLICATION NUMBER: US/10/825,603
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 60/463,042
; PRIOR FILING DATE: 2003-04-16
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 3
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-825-603-3

Query Match 100.0%; Score 28; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLSYSR 6

Db 1 VLSYSR 6

RESULT 2

US-09-852-424-17
; Sequence 17, Application US/09852424
; Patent No. US20020156034A1
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia; and
; APPLICANT: Chemokine Therapeutics Corporation
; TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS
; FILE REFERENCE: 80021-257
; CURRENT APPLICATION NUMBER: US/09/852,424
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: CA 2,305,787
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 60/205,467
; PRIOR FILING DATE: 2000-05-19

```

; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Engineered in
; NAME/KEY: SITE
; LOCATION: (8)
; OTHER INFORMATION: binds with residue at position 9 of SEQ ID NO 16
US-09-852-424-17

Query Match          100.0%; Score 28; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLSYR 6
   |||||
Db 3 VLSYR 8

RESULT 3
US-09-852-424-131
; Sequence 131, Application US/09852424
; Patent No. US20020156034A1
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia; and
; APPLICANT: Chemokine Therapeutics Corporation
; TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS
; FILE REFERENCE: 80021-257
; CURRENT APPLICATION NUMBER: US/09/852,424
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: CA 2,305,787
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 60/205,467
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 131
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (8)
; OTHER INFORMATION: Binds to the residue at position 9 on SEQ ID NO
; OTHER INFORMATION: 130.
; OTHER INFORMATION: Description of Artificial Sequence: Engineered in
; OTHER INFORMATION: Laboratory
US-09-852-424-131

Query Match          100.0%; Score 28; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLSYR 6
   |||||
Db 3 VLSYR 8

RESULT 4
US-09-835-107-11
; Sequence 11, Application US/09835107
; Patent No. US20020165123A1
; GENERAL INFORMATION:
; APPLICANT: Tudan, Christopher R.
; APPLICANT: Merzouk, Ahmed
; APPLICANT: Arab, Lakhdar
; APPLICANT: Saxena, Geeta
; APPLICANT: Eaves, Connie J.
; APPLICANT: Cashman, Johanne
; APPLICANT: Salari, Hassan
; TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS
; FILE REFERENCE: SMAR012
; CURRENT APPLICATION NUMBER: US/09/835,107
; CURRENT FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: CA 2,305,036
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/232,425
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: CA 2,335,109
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (8)
; OTHER INFORMATION: bonds with SEQ ID NO 31 by forming lysine bridge
; OTHER INFORMATION: dimer between each arg of each position 8 of SEQ
; OTHER INFORMATION: ID NO 31 and SEQ ID NO 32
; OTHER INFORMATION: Synthesised in Laboratory: SDF-1(1-8)2-lysine
; OTHER INFORMATION: bridge dimer: or CTCE9904
US-09-835-107-32

Query Match          100.0%; Score 28; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

; APPLICANT: Clark-Lewis
; APPLICANT: Salari, Hassan
; TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS
; FILE REFERENCE: SMAR012
; CURRENT APPLICATION NUMBER: US/09/835,107
; CURRENT FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: CA 2,305,036
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/232,425
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: CA 2,335,109
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesised in Laboratory
US-09-835-107-11

Query Match          100.0%; Score 28; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLSYR 6
   |||||
Db 3 VLSYR 8

RESULT 5
US-09-835-107-32
; Sequence 32, Application US/09835107
; Patent No. US20020165123A1
; GENERAL INFORMATION:
; APPLICANT: Tudan, Christopher R.
; APPLICANT: Merzouk, Ahmed
; APPLICANT: Arab, Lakhdar
; APPLICANT: Saxena, Geeta
; APPLICANT: Eaves, Connie J.
; APPLICANT: Cashman, Johanne
; APPLICANT: Clark-Lewis
; APPLICANT: Salari, Hassan
; TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS
; FILE REFERENCE: SMAR012
; CURRENT APPLICATION NUMBER: US/09/835,107
; CURRENT FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: CA 2,305,036
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/232,425
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: CA 2,335,109
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (8)
; OTHER INFORMATION: bonds with SEQ ID NO 31 by forming lysine bridge
; OTHER INFORMATION: dimer between each arg of each position 8 of SEQ
; OTHER INFORMATION: ID NO 31 and SEQ ID NO 32
; OTHER INFORMATION: Synthesised in Laboratory: SDF-1(1-8)2-lysine
; OTHER INFORMATION: bridge dimer: or CTCE9904
US-09-835-107-32

Query Match          100.0%; Score 28; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```


QY 1 VLSYR 6
| | | | |
Db 3 VLSYR 8

RESULT 6

US-10-086-177A-11
; Sequence 11, Application US/10086177A
; Publication No. US20030148940A1
; GENERAL INFORMATION:
; APPLICANT: Tudan, Christopher R.
; APPLICANT: Merzouk, Ahmed
; APPLICANT: Saxena, Geeta
; APPLICANT: Eaves, Connie J.
; APPLICANT: Cashman, Johanne
; APPLICANT: Clark-Lewis, Ian
; APPLICANT: Salari, Hassan
; TITLE OF INVENTION: CXCR Agonist Treatment of Hematopoietic
; TITLE OF INVENTION: Cells
; FILE REFERENCE: SMAR-012CIP
; CURRENT APPLICATION NUMBER: US/10/086,177A
; CURRENT FILING DATE: 2002-02-26
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/232,425
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: CA 2,305,036
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: CA 2,335,109
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized in Laboratory
US-10-086-177A-11

Query Match 100.0%; Score 28; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLSYR 6
| | | | |
Db 3 VLSYR 8

RESULT 7

US-10-086-177A-32
; Sequence 32, Application US/10086177A
; Publication No. US20030148940A1
; GENERAL INFORMATION:
; APPLICANT: Tudan, Christopher R.
; APPLICANT: Merzouk, Ahmed
; APPLICANT: Saxena, Geeta
; APPLICANT: Eaves, Connie J.
; APPLICANT: Cashman, Johanne
; APPLICANT: Clark-Lewis, Ian
; APPLICANT: Salari, Hassan
; TITLE OF INVENTION: CXCR Agonist Treatment of Hematopoietic
; TITLE OF INVENTION: Cells
; FILE REFERENCE: SMAR-012CIP
; CURRENT APPLICATION NUMBER: US/10/086,177A
; CURRENT FILING DATE: 2002-02-26
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/232,425
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: CA 2,305,036
; PRIOR FILING DATE: 2000-04-12

; PRIOR APPLICATION NUMBER: CA 2,335,109
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized in Laboratory: SDF-1 (1-8)2-lysine
; OTHER INFORMATION: bridge dimer: CTCE9904
US-10-086-177A-32

Query Match 100.0%; Score 28; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLSYR 6
| | | | |
Db 3 VLSYR 8

RESULT 8

US-10-222-703A-805
; Sequence 805, Application US/10222703A
; Publication No. US20050059584A1
; GENERAL INFORMATION:
; APPLICANT: MERZOUK, AHMED
; APPLICANT: HABI, ABDELKRIM
; APPLICANT: WONG, DONALD
; APPLICANT: SALARI, HASSAN
; TITLE OF INVENTION: NOVEL CHEMOKINE MIMETICS SYNTHESIS AND THEIR USE
; FILE REFERENCE: 592960-00002
; CURRENT APPLICATION NUMBER: US/10/222,703A
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: 10/086,177
; PRIOR FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: 09/835,107
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/373,629
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/373,628
; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 868
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 805
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-222-703A-805

Query Match 100.0%; Score 28; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLSYR 6
| | | | |
Db 3 VLSYR 8

RESULT 9

US-09-852-424-14
; Sequence 14, Application US/09852424
; Patent No. US20020156034A1
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia; and
; APPLICANT: Chemokine Therapeutics Corporation
; TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS
; FILE REFERENCE: 80021-257
; CURRENT APPLICATION NUMBER: US/09/852,424
; CURRENT FILING DATE: 2001-09-26

; FILE REFERENCE: 80021-257
; CURRENT APPLICATION NUMBER: CA 2,305,787
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/205,467
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Engineered in
; OTHER INFORMATION: Laboratory
US-09-852-424-14

Query Match 100.0%; Score 28; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLSYR 6
| | | | |
Db 3 VLSYR 8

RESULT 10
US-09-852-424-15
; Sequence 15, Application US/09852424
; Patent No. US20020156034A1
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia; and
; APPLICANT: Chemokine Therapeutics Corporation
; TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS
; FILE REFERENCE: 80021-257
; CURRENT APPLICATION NUMBER: US/09/852,424
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: CA 2,305,787
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 60/205,467
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (9)
; OTHER INFORMATION: dimer of amino acids 1-9 in which the amino acid
; OTHER INFORMATION: chains are joined by a disulphide bond between
; OTHER INFORMATION: each of the cysteines at position 9 in each
; OTHER INFORMATION: sequence.
; OTHER INFORMATION: Description of Artificial Sequence: Engineered in
; OTHER INFORMATION: Laboratory (SDF-1 (1-9)2 [P2G])
US-09-852-424-15

Query Match 100.0%; Score 28; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLSYR 6
| | | | |
Db 3 VLSYR 8

RESULT 11
US-09-852-424-16
; Sequence 16, Application US/09852424
; Patent No. US20020156034A1
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia; and
; APPLICANT: Chemokine Therapeutics Corporation
; TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS

; FILE REFERENCE: 80021-257
; CURRENT APPLICATION NUMBER: US/09/852,424
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: CA 2,305,787
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 60/205,467
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (9)
; OTHER INFORMATION: Xaa=an amino acid like lysine; ornithine or any
; OTHER INFORMATION: other natural or unnatural amino acid serving as a
; OTHER INFORMATION: linker between each of the arginines at position 8
; OTHER INFORMATION: in each of SEQ ID NOS 16 and 17.
; OTHER INFORMATION: Description of Artificial Sequence: Engineered in
; OTHER INFORMATION: Laboratory (SDF-1(1-8)2[P2G])
US-09-852-424-16

Query Match 100.0%; Score 28; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLSYR 6
| | | | |
Db 3 VLSYR 8

RESULT 12
US-09-852-424-130
; Sequence 130, Application US/09852424
; Patent No. US20020156034A1
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia; and
; APPLICANT: Chemokine Therapeutics Corporation
; TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS
; FILE REFERENCE: 80021-257
; CURRENT APPLICATION NUMBER: US/09/852,424
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: CA 2,305,787
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 60/205,467
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 130
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (9)
; OTHER INFORMATION: AMIDATION; acts as a linking moiety between each
; OTHER INFORMATION: arginine at position 8 in each of SEQ ID 130 and
; OTHER INFORMATION: SEQ ID 131.
; OTHER INFORMATION: Description of Artificial Sequence: Engineered in
; OTHER INFORMATION: Laboratory
US-09-852-424-130

Query Match 100.0%; Score 28; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLSYR 6
| | | | |
Db 3 VLSYR 8

```
RESULT 13
US-09-852-424-132
; Sequence 132, Application US/09852424
; Patent No. US20020156034A1
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia; and
; APPLICANT: Chemokine Therapeutics Corporation
; TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS
; FILE REFERENCE: 80021-257
; CURRENT APPLICATION NUMBER: US/09/852,424
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: CA 2,305,787
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 60/205,467
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 132
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (9)
; OTHER INFORMATION: AMIDATION
; OTHER INFORMATION: Description of Artificial Sequence: Engineered in
; OTHER INFORMATION: Laboratory
; NAME/KEY: DISULFID
; LOCATION: (9)
; OTHER INFORMATION: dimer of amino acids 1-9 in which the amino acid
; OTHER INFORMATION: chains are joined by a disulphide bond between
; OTHER INFORMATION: each of the amidated cysteines at position 9 in
; OTHER INFORMATION: each sequence.
US-09-852-424-132
Query Match 100.0%; Score 28; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLSYSR 6
DB 3 VLSYSR 8

RESULT 14
US-09-835-107-6
; Sequence 6, Application US/09835107
; Patent No. US20020165123A1
; GENERAL INFORMATION:
; APPLICANT: Tudan, Christopher R.
; APPLICANT: Merzouk, Ahmed
; APPLICANT: Arab, Lakhdar
; APPLICANT: Saxena, Geeta
; APPLICANT: Eaves, Connie J.
; APPLICANT: Cashman, Johanne
; APPLICANT: Clark-Lewis
; APPLICANT: Salari, Hassan
; TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS
; FILE REFERENCE: SMAR012
; CURRENT APPLICATION NUMBER: US/09/835,107
; CURRENT FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: CA 2,305,036
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/232,425
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: CA 2,335,109
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (9)
; OTHER INFORMATION: Disulphide linkage between each cys at position 9
; OTHER INFORMATION: of each monomer.
; OTHER INFORMATION: Synthesised in Laboratory:
; OTHER INFORMATION: SDP-1(1-9)2-C9/C9-cysteine dimer: or CTCE9901
US-09-835-107-6
Query Match 100.0%; Score 28; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLSYSR 6
DB 3 VLSYSR 8

RESULT 15
US-09-835-107-7
; Sequence 7, Application US/09835107
; Patent No. US20020165123A1
; GENERAL INFORMATION:
; APPLICANT: Tudan, Christopher R.
; APPLICANT: Merzouk, Ahmed
; APPLICANT: Arab, Lakhdar
; APPLICANT: Saxena, Geeta
; APPLICANT: Eaves, Connie J.
; APPLICANT: Cashman, Johanne
; APPLICANT: Clark-Lewis
; APPLICANT: Salari, Hassan
; TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS
; FILE REFERENCE: SMAR012
; CURRENT APPLICATION NUMBER: US/09/835,107
; CURRENT FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: CA 2,305,036
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/232,425
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: CA 2,335,109
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (9)
; OTHER INFORMATION: Disulphide linkage between each cys at position 9
; OTHER INFORMATION: of each monomer.
; OTHER INFORMATION: Synthesised in Laboratory:
; OTHER INFORMATION: SDP-1(1-9)2-C9/C9-cysteine dimer: or CTCE9901
US-09-835-107-7
Query Match 100.0%; Score 28; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLSYSR 6
DB 3 VLSYSR 8

Search completed: August 10, 2006, 23:19:37
Job time : 69.0909 secs
```

THIS PAGE BLANK (USPTO)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 10, 2006, 23:13:11 ; Search time 10.9091 Seconds
(without alignments)
37.022 Million cell updates/sec

Title: US-10-825-603-3

Perfect score: 28

Sequence: 1 VLSYR 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 239914 seqs, 67312017 residues

Total number of hits satisfying chosen parameters: 239914

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New.*

- 1: /EMC Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 2: /EMC Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 3: /EMC Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 4: /EMC Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 5: /EMC Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 6: /EMC Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 7: /EMC Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 8: /EMC Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	100.0	93	US-10-505-928-112	Sequence 112, App
2	28	100.0	93	US-10-511-937-2454	Sequence 2454, App
3	28	100.0	168	US-10-449-902-55009	Sequence 55009, A
4	28	100.0	607	US-10-449-902-47399	Sequence 47399, A
5	26	92.9	556	US-10-449-902-55969	Sequence 55969, A
6	26	92.9	608	US-10-449-902-55390	Sequence 55390, A
7	25	89.3	170	US-10-953-349-26849	Sequence 26849, A
8	25	89.3	256	US-10-953-349-19900	Sequence 19900, A
9	25	89.3	354	US-10-953-349-19899	Sequence 19899, A
10	25	89.3	354	US-11-330-403-14326	Sequence 14326, A
11	25	89.3	439	US-10-953-349-19898	Sequence 19898, A
12	25	89.3	1049	US-10-449-902-41588	Sequence 41588, A
13	24	85.7	135	US-11-324-947-2	Sequence 2, Appli
14	24	85.7	186	US-11-056-355B-17852	Sequence 17852, A
15	24	85.7	212	US-11-056-355B-84755	Sequence 84755, A
16	24	85.7	272	US-11-199-489A-56	Sequence 56, Appl
17	24	85.7	283	US-11-330-403-11448	Sequence 11448, A
18	24	85.7	289	US-11-330-403-5129	Sequence 5129, Ap
19	24	85.7	295	US-11-056-355B-81758	Sequence 81758, A
20	24	85.7	309	US-11-056-355B-84754	Sequence 84754, A
21	24	85.7	310	US-11-056-355B-84753	Sequence 84753, A
22	24	85.7	319	US-10-449-902-55814	Sequence 55814, A
23	24	85.7	330	US-10-449-902-37163	Sequence 37163, A
24	24	85.7	346	US-11-056-355B-85910	Sequence 85910, A
25	24	85.7	360	US-11-056-355B-81757	Sequence 81757, A

26	24	85.7	362	7	US-11-056-355B-55170	Sequence 55170, A
27	24	85.7	382	7	US-11-056-355B-81756	Sequence 81756, A
28	24	85.7	385	7	US-11-289-102-375	Sequence 375, App
29	24	85.7	410	7	US-11-056-355B-55169	Sequence 55169, A
30	24	85.7	425	7	US-11-056-355B-100537	Sequence 100537, A
31	24	85.7	425	7	US-11-056-355B-111776	Sequence 111776, A
32	24	85.7	453	6	US-10-953-349-24099	Sequence 24099, A
33	24	85.7	467	7	US-11-056-355B-90015	Sequence 90015, A
34	24	85.7	467	7	US-11-056-355B-93771	Sequence 93771, A
35	24	85.7	507	6	US-10-953-349-3543	Sequence 3543, Ap
36	24	85.7	507	7	US-11-056-355B-30284	Sequence 30284, A
37	24	85.7	507	7	US-11-056-355B-33874	Sequence 33874, A
38	24	85.7	507	7	US-11-056-355B-77565	Sequence 77565, A
39	24	85.7	507	7	US-11-056-355B-104817	Sequence 104817, A
40	24	85.7	507	7	US-11-056-355B-116056	Sequence 116056, A
41	24	85.7	514	6	US-10-449-902-46935	Sequence 46935, A
42	24	85.7	516	7	US-11-056-355B-100536	Sequence 100536, A
43	24	85.7	516	7	US-11-056-355B-111775	Sequence 111775, A
44	24	85.7	524	6	US-10-953-349-24098	Sequence 24098, A
45	24	85.7	526	7	US-11-056-355B-100535	Sequence 100535, A

ALIGNMENTS

RESULT 1

US-10-505-928-112
; Sequence 112, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 112
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-112

Query Match 100.0%; Score 28; DB 6; Length 93;
Best Local Similarity 100.0%; Pred. No. 8.7;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLSYR 6
|||
DB 24 VLSYR 29

RESULT 2

US-10-511-937-2454
; Sequence 2454, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946

; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2454
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-937-2454

Query Match 100.0%; Score 28; DB 6; Length 93;
Best Local Similarity 100.0%; Pred. No. 8.7; 0; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;

QY 1 VLSYR 6
Db 24 VLSYR 29
|||||

RESULT 3

US-10-449-902-55009
; Sequence 55009, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55009
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-55009

Query Match 100.0%; Score 28; DB 6; Length 168;
Best Local Similarity 100.0%; Pred. No. 16; 0; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;

QY 1 VLSYR 6
Db 73 VLSYR 78
|||||

RESULT 4

US-10-449-902-47399
; Sequence 47399, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11

; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47399
; LENGTH: 607
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-47399

Query Match 100.0%; Score 28; DB 6; Length 607;
Best Local Similarity 100.0%; Pred. No. 62; 0; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;

QY 1 VLSYR 6
Db 73 VLSYR 78
|||||

RESULT 5

US-10-449-902-55969
; Sequence 55969, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55969
; LENGTH: 556
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-55969

Query Match 92.9%; Score 26; DB 6; Length 556;
Best Local Similarity 83.3%; Pred. No. 1.8e+02; 0; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0;

QY 1 VLSYR 6
Db 158 VLSYR 163
|||||

RESULT 6

US-10-449-902-55390
; Sequence 55390, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55390
; LENGTH: 608
; TYPE: PRT

```
; ORGANISM: Oryza sativa
US-10-449-902-55390

Query Match      92.9%; Score 26; DB 6; Length 608;
Best Local Similarity 83.3%; Pred. No. 1.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 VLSLYR 6
      ||:||||
Db      198 VLSYR 203

RESULT 7
US-10-953-349-26849
; Sequence 26849, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 26849
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-953-349-26849

Query Match      89.3%; Score 25; DB 6; Length 170;
Best Local Similarity 83.3%; Pred. No. 89;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 VLSLYR 6
      ||:||||
Db      34 VLSYR 39

RESULT 8
US-10-953-349-19900
; Sequence 19900, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 19900
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-19900

Query Match      89.3%; Score 25; DB 6; Length 256;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 VLSLYR 6
      ||:||||
Db      211 VSLAYR 216

RESULT 9
US-10-953-349-19899
; Sequence 19899, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
```

```
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 19899
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-19899
```

```
Query Match      89.3%; Score 25; DB 6; Length 300;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 VLSLYR 6
      ||:||||
Db      255 VSLAYR 260
```

```
RESULT 10
US-11-330-403-14326
; Sequence 14326, Application US/11330403
; Publication No. US20060159563A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53629)B
; CURRENT APPLICATION NUMBER: US/11/330,403
; CURRENT FILING DATE: 2006-01-12
; NUMBER OF SEQ ID NOS: 19250
; SEQ ID NO 14326
; LENGTH: 354
; TYPE: PRT
; ORGANISM: Ustilago maydis 521
US-11-330-403-14326
```

```
Query Match      89.3%; Score 25; DB 7; Length 354;
Best Local Similarity 83.3%; Pred. No. 1.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 VLSLYR 6
      ||:||||
Db      44 VSLNYR 49
```

```
RESULT 11
US-10-953-349-19898
; Sequence 19898, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 19898
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-19898
```

```
Query Match      89.3%; Score 25; DB 6; Length 439;
Best Local Similarity 83.3%; Pred. No. 2.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 VLSLYR 6
```

Db 394 VSLAYR 399
|||:|

RESULT 12
US-10-449-902-41588
; Sequence 41588, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41588
; LENGTH: 1049
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-41588

Query Match 89.3%; Score 25; DB 6; Length 1049;
Best Local Similarity 83.3%; Pred. No. 6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLSLYR 6
|:||||

Db 731 VALSYR 736

RESULT 13
US-11-324-947-2
; Sequence 2, Application US/11324947
; Publication No. US20060105396A1
; GENERAL INFORMATION:
; APPLICANT: HIATT, ANDREW C.
; APPLICANT: HEIN, MICHAEL B.
; APPLICANT: FITCHEN, JOHN H.
; TITLE OF INVENTION: J CHAIN POLYPEPTIDE TARGETING MOLECULE LINKED TO AN IMAGING AGENT
; FILE REFERENCE: EPI3003C
; CURRENT APPLICATION NUMBER: US/11/324,947
; CURRENT FILING DATE: 2006-01-04
; PRIOR APPLICATION NUMBER: US/10/062,467
; PRIOR FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: 08/782,480
; PRIOR FILING DATE: 1997-01-10
; PRIOR APPLICATION NUMBER: 09/005,167
; PRIOR FILING DATE: 1998-01-09
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Mus sp.
US-11-324-947-2

Query Match 85.7%; Score 24; DB 7; Length 135;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLSLYR 6
|:||||

Db 112 VKLSYR 117

RESULT 14
US-11-056-355B-17852
; Sequence 17852, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 17852
; LENGTH: 186
; TYPE: prt
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(186)
; OTHER INFORMATION: Ceres Seq. ID no. 12363377
US-11-056-355B-17852

Query Match 85.7%; Score 24; DB 7; Length 186;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SLSYR 6
|:||||

Db 181 SLSYR 185

RESULT 15
US-11-056-355B-84755
; Sequence 84755, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 84755
; LENGTH: 212
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(212)
; OTHER INFORMATION: Ceres Seq. ID no. 12676738
US-11-056-355B-84755

Query Match 85.7%; Score 24; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SLSYR 6
|:||||

Db 16 SLSYR 20

Search completed: August 10, 2006, 23:20:44
Job time : 11.9091 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 10, 2006, 23:10:21 ; Search time 32.1818 Seconds
(without alignments)
24.479 Million cell updates/sec

Title: US-10-825-603-5

Perfect score: 43

Sequence: 1 RVSLSYRF 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /EMC Celerra_SIDS3/ptodata/2/iaa/5 COMB.pcp.*
- 2: /EMC Celerra_SIDS3/ptodata/2/iaa/6 COMB.pcp.*
- 3: /EMC Celerra_SIDS3/ptodata/2/iaa/7 COMB.pcp.*
- 4: /EMC Celerra_SIDS3/ptodata/2/iaa/H COMB.pcp.*
- 5: /EMC Celerra_SIDS3/ptodata/2/iaa/PCTUS COMB.pcp.*
- 6: /EMC Celerra_SIDS3/ptodata/2/iaa/RE COMB.pcp.*
- 7: /EMC Celerra_SIDS3/ptodata/2/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	35	81.4	55	2	US-09-270-767-39075 Sequence 39075, A
2	35	81.4	55	2	US-09-270-767-54292 Sequence 54292, A
3	32	74.4	70	2	US-09-248-796A-23114 Sequence 23114, A
4	32	74.4	396	2	US-10-094-749-2492 Sequence 2492, Ap
5	32	74.4	445	2	US-10-104-047-2209 Sequence 2209, Ap
6	32	74.4	859	2	US-09-708-200-7 Sequence 7, Appli
7	32	74.4	859	2	US-09-788-657-16 Sequence 16, Appli
8	32	74.4	859	2	US-09-712-691-5 Sequence 5, Appli
9	32	74.4	859	2	US-09-707-468C-5 Sequence 5, Appli
10	32	74.4	859	2	US-10-641-068-16 Sequence 16, Appli
11	32	74.4	859	2	US-09-760-285-14 Sequence 14, Appli
12	31	72.1	336	2	US-09-902-540-11471 Sequence 11471, A
13	31	72.1	406	2	US-09-543-681A-4268 Sequence 4268, Ap
14	31	72.1	708	2	US-09-252-991A-25303 Sequence 25303, A
15	30	69.8	9	2	US-09-646-193-2 Sequence 2, Appli
16	30	69.8	9	2	US-09-646-193-3 Sequence 3, Appli
17	30	69.8	9	2	US-09-646-192-2 Sequence 2, Appli
18	30	69.8	9	2	US-09-646-192-3 Sequence 3, Appli
19	30	69.8	10	2	US-09-646-193-4 Sequence 4, Appli
20	30	69.8	86	2	US-09-646-192-4 Sequence 4, Appli
21	30	69.8	86	2	US-09-252-991A-20089 Sequence 20089, A
22	30	69.8	90	2	US-09-134-001C-5426 Sequence 5426, Ap
23	30	69.8	250	2	US-09-270-767-35537 Sequence 35537, A
24	30	69.8	250	2	US-09-270-767-50754 Sequence 50754, A
25	30	69.8	262	2	US-09-252-991A-25231 Sequence 25231, A
26	30	69.8	268	2	US-09-252-991A-30879 Sequence 30879, A

27	30	69.8	360	2	US-09-489-039A-13055 Sequence 13055, A
28	30	69.8	364	2	US-09-418-980-8 Sequence 8, Appli
29	30	69.8	364	2	US-09-809-665A-151 Sequence 151, Appl
30	30	69.8	364	2	US-09-506-078-45 Sequence 45, Appl
31	30	69.8	438	1	US-08-282-197C-59 Sequence 59, Appl
32	30	69.8	567	2	US-10-172-527A-7 Sequence 7, Appli
33	30	69.8	567	3	US-11-120-422-7 Sequence 7, Appli
34	30	69.8	568	2	US-09-469-200E-10 Sequence 10, Appli
35	30	69.8	568	2	US-10-011-768B-10 Sequence 10, Appli
36	30	69.8	588	5	PCT-US95-13749-4 Sequence 4, Appli
37	30	69.8	712	1	US-08-121-713D-64 Sequence 64, Appl
38	30	69.8	712	1	US-08-835-268-64 Sequence 64, Appl
39	30	69.8	712	1	US-09-060-692-64 Sequence 64, Appl
40	30	69.8	712	2	US-08-833-391-64 Sequence 64, Appl
41	30	69.8	712	2	US-09-060-610-64 Sequence 64, Appl
42	30	69.8	712	5	PCT-US94-10151A-64 Sequence 64, Appl
43	30	69.8	1426	2	US-09-136-574A-43 Sequence 43, Appl
44	29	67.4	8	2	US-09-430-470-18 Sequence 18, Appl
45	29	67.4	12	2	US-09-132-521-2 Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-09-270-767-39075
; Sequence 39075, Application US/09270767
; Patent No. 6703491

; GENERAL INFORMATION:
; APPLICANT: Homburger et al.

; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17

; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 39075

; LENGTH: 55

; TYPE: PRT

; ORGANISM: Drosophila melanogaster

US-09-270-767-39075

Query Match 81.4%; Score 35; DB 2; Length 55;

Best Local Similarity 87.5%; Pred. No. 3.2;

Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SVSLSYRF 9

Db 15 SVSLSYRF 22

RESULT 2

US-09-270-767-54292
; Sequence 54292, Application US/09270767
; Patent No. 6703491

; GENERAL INFORMATION:
; APPLICANT: Homburger et al.

; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17

; NUMBER OF SEQ ID NOS: 62517

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 54292

; LENGTH: 55

; TYPE: PRT

; ORGANISM: Drosophila melanogaster

US-09-270-767-54292

Query Match 81.4%; Score 35; DB 2; Length 55;

Best Local Similarity 87.5%; Pred. No. 3.2;

Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy      2 SVSLSYRF 9
Db      15 SLSLSYRF 22

RESULT 3
US-09-248-796A-23114
; Sequence 23114, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 23114
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-23114

Query Match      74.4%; Score 32; DB 2; Length 70;
Best Local Similarity 55.6%; Pred. No. 18;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy      1 RSVLSYRF 9
Db      46 RDIALNYRF 54

RESULT 4
US-10-094-749-2492
; Sequence 2492, Application US/10094749
; Patent No. 6979557
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHIKO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOKYU
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: NOVEL FULL-LENGTH cDNA
; FILE REFERENCE: 084335/0160
; CURRENT APPLICATION NUMBER: US/10/094,749
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/350,435
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: JP 2001-328381
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 3381
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2492
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Homo sapiens
```

```
US-10-094-749-2492

Query Match      74.4%; Score 32; DB 2; Length 396;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 RSVLSYRF 9
Db      188 RPSVVTYRF 196

RESULT 5
US-10-104-047-2209
; Sequence 2209, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: NO. 6943241e1 full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2209
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-2209

Query Match      74.4%; Score 32; DB 2; Length 445;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 RSVLSYRF 9
Db      237 RPSVVTYRF 245

RESULT 6
US-09-708-200-7
; Sequence 7, Application US/09708200
; Patent No. 6576468
; GENERAL INFORMATION:
; APPLICANT: Nicolaides, Nicholas C
; APPLICANT: Grasso, Luigi
; APPLICANT: Sasse, Philip M
; TITLE OF INVENTION: METHODS FOR ISOLATING NOVEL ANTIMICROBIAL AGENTS FROM
; FILE OF INVENTION: HYPERMUTABLE CELLS
; FILE REFERENCE: MOR-0005
; CURRENT APPLICATION NUMBER: US/09/708,200
; CURRENT FILING DATE: 2000-11-07
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 859
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-708-200-7

Query Match      74.4%; Score 32; DB 2; Length 859;
Best Local Similarity 77.8%; Pred. No. 2.8e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 RSVLSYRF 9
Db      301 RSLSLMRF 309

RESULT 7
US-09-788-657-16
; Sequence 16, Application US/09788657
```

; Patent No. 6656736
; GENERAL INFORMATION:
; APPLICANT: Nicolaides, Nicholas
; APPLICANT: Sasse, Philip
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Grasso, Luigi
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Methods for generating hypermutable
; FILE REFERENCE: 01107.00097
; CURRENT APPLICATION NUMBER: US/09/788,657
; CURRENT FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 60/184,336
; PRIOR FILING DATE: 2000-02-23
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 859
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-788-657-16

Query Match 74.4%; Score 32; DB 2; Length 859;
Best Local Similarity 77.8%; Pred. No. 2.8e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RSVLSYRF 9
||:|||||
Db 301 RSLSLSMRF 309

RESULT 8
US-09-712-691-5
; Sequence 5, Application US/09712691
; Patent No. 6737268
; GENERAL INFORMATION:
; APPLICANT: Nicolaides, Nicholas C
; APPLICANT: Grasso, Luigi
; APPLICANT: Sasse, Philip M
; TITLE OF INVENTION: METHODS FOR GENERATING GENETICALLY ALTERED ANTIGENS
; FILE REFERENCE: MOR-0015
; CURRENT APPLICATION NUMBER: US/09/712,691
; CURRENT FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 859
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-712-691-5

Query Match 74.4%; Score 32; DB 2; Length 859;
Best Local Similarity 77.8%; Pred. No. 2.8e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RSVLSYRF 9
||:|||||
Db 301 RSLSLSMRF 309

RESULT 9
US-09-707-468C-5
; Sequence 5, Application US/09707468C
; Patent No. 6808894
; GENERAL INFORMATION:
; APPLICANT: Nicolaides, Nicholas C.
; APPLICANT: Grasso, Luigi
; APPLICANT: Sasse, Philip M.
; TITLE OF INVENTION: Methods For Generating Genetically Altered Antibody-Producing
; TITLE OF INVENTION: Cell Lines With Improved Antibody Characteristics
; FILE REFERENCE: MOR-0003
; CURRENT APPLICATION NUMBER: US/09/707,468C
; CURRENT FILING DATE: 2000-11-07

; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 859
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-707-468C-5

Query Match 74.4%; Score 32; DB 2; Length 859;
Best Local Similarity 77.8%; Pred. No. 2.8e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RSVLSYRF 9
||:|||||
Db 301 RSLSLSMRF 309

RESULT 10
US-10-641-068-16
; Sequence 16, Application US/10641068
; Patent No. 6921666
; GENERAL INFORMATION:
; APPLICANT: Nicolaides, Nicholas
; APPLICANT: Sasse, Philip
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Grasso, Luigi
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Methods for generating hypermutable
; FILE REFERENCE: 01107.00097
; CURRENT APPLICATION NUMBER: US/10/641,068
; CURRENT FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: US/09/788,657
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 60/184,336
; PRIOR FILING DATE: 2000-02-23
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 859
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-641-068-16

Query Match 74.4%; Score 32; DB 2; Length 859;
Best Local Similarity 77.8%; Pred. No. 2.8e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RSVLSYRF 9
||:|||||
Db 301 RSLSLSMRF 309

RESULT 11
US-09-760-285-14
; Sequence 14, Application US/09760285
; Patent No. 6982169
; GENERAL INFORMATION:
; APPLICANT: Nicolaides, Nicholas C
; APPLICANT: Grasso, Luigi
; APPLICANT: Sasse, Philip M
; TITLE OF INVENTION: CHEMICAL INHIBITORS OF MISMATCH REPAIR
; FILE REFERENCE: MOR-0017
; CURRENT APPLICATION NUMBER: US/09/760,285
; CURRENT FILING DATE: 2001-01-15
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 859
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-760-285-14

```

Query Match          74.4%; Score 32; DB 2; Length 859;
Best Local Similarity 77.8%; Pred. No. 2.8e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RSVLSYR 9
DB 301 RSLSLMR 309

RESULT 12
US-09-902-540-11471
; Sequence 11471, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 11471
; LENGTH: 336
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-11471

Query Match          72.1%; Score 31; DB 2; Length 336;
Best Local Similarity 75.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSVLSYR 8
DB 35 RAVSLNYR 42

RESULT 13
US-09-543-681A-4268
; Sequence 4268, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 4268
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-4268

Query Match          72.1%; Score 31; DB 2; Length 406;
Best Local Similarity 66.7%; Pred. No. 2e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RSVLSYR 9
DB 206 RGLPLSYR 214

RESULT 14
US-09-252-991A-25303
; Sequence 25303, Application US/09252991A
; Patent No. 6551795

```

```

; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 25303
; LENGTH: 708
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25303

Query Match          72.1%; Score 31; DB 2; Length 708;
Best Local Similarity 85.7%; Pred. No. 3.7e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 VLSYR 9
DB 530 LSLSYR 536

RESULT 15
US-09-646-193-2
; Sequence 2, Application US/09646193
; Patent No. 6875738
; GENERAL INFORMATION:
; APPLICANT: Clark-Lewis, Ian
; APPLICANT: Duronio, Vincent
; APPLICANT: Salari, Hassan
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: Therapeutic Chemokine Receptor Antagonists
; FILE REFERENCE: 080353-000000US
; CURRENT APPLICATION NUMBER: US/09/646,193
; CURRENT FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: CA 2,245,224
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: WO PCT/CA99/00221
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: WO PCT/CA99/00750
; PRIOR FILING DATE: 1999-08-16
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CXCR4
; OTHER INFORMATION: antagonist peptide compound N-terminal sequence
; NAME/KEY: MOD_RES
; LOCATION: (9)
; OTHER INFORMATION: Xaa = Cys or Cys modified by a polypeptide
; OTHER INFORMATION: homologous to a portion of SDF-1
US-09-646-193-2

Query Match          69.8%; Score 30; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 5e+05;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RSVLSYR 8
DB 1 KGVLSYR 8

Search completed: August 10, 2006, 23:13:11
Job time : 33.1818 secs

```

THIS PAGE BLANK (USPTO)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 10, 2006, 22:53:25 ; Search time 150 Seconds
(without alignments)

55.501 Million cell updates/sec

Title: US-10-825-603-5

Perfect score: 43

Sequence: 1 RVSLSYRF 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 7.2.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	37	86.0	350	Q2RSU4_RHURU	Q2rsu4 rhodospiril
2	37	86.0	1356	Q5MQD0_9CORO	Q5mqd0 human coron
3	35	81.4	165	Q9LSS1_ARATH	Q9lss1 arabidopsis
4	35	81.4	218	Q34VG2_9GAMM	Q34vg2 alkalinimi
5	35	81.4	322	Q5EGW8_9POXV	Q5egw8 goatpox vir
6	35	81.4	468	Q23425_ARATH	Q23425 arabidopsis
7	35	81.4	1125	Q5LDR9_BACFN	Q5ldr9 bacteroides
8	35	81.4	1125	Q93TH9_BACFR	Q93th9 bacteroides
9	34	79.1	333	Q3GT8_9DELT	Q3gt8 pelobacter
10	34	79.1	366	Q6D6D4_ERWCT	Q6d6d4 erwinia car
11	34	79.1	367	Q9RM69_ERWCA	Q9rm69 erwinia car
12	34	79.1	372	Q4BPU4_BURVI	Q4bpu4 burkholderi
13	34	79.1	403	Q96773_HAEDU	Q96773 haemophilus
14	34	79.1	433	Q2S253_SSPHI	Q2s253 salinibacte
15	34	79.1	559	Q9DQ91_9CLOS	Q9dq91 pineapple m
16	34	79.1	705	Q4Q9U3_LEIMA	Q4q9u3 leishmania
17	34	79.1	932	Q2R0G4_ORYSA	Q2r0g4 oryza sativ
18	34	79.1	6733	Q3T8J2_9NIDO	Q3t8j2 breda virus
19	33	76.7	154	Q6MAQ2_PARUM	Q6maq2 parachlamyd
20	33	76.7	262	Q6CYK2_ERWCT	Q6cyk2 erwinia car
21	33	76.7	299	Q9RBF7_RALEU	Q9rbf7 ralatonia e
22	33	76.7	387	Q7QBV3_ANOGA	Q7qbv3 anopheles g
23	33	76.7	391	Q8DTD9_STRMU	Q8dtd9 streptococ
24	33	76.7	405	Q6FRG7_CANGA	Q6frg7 candida gla
25	33	76.7	456	Q3CKF4_THBET	Q3ckf4 thermoanaer
26	33	76.7	505	Q5L215_GEOKA	Q5l215 geobacillus
27	33	76.7	652	Q3P7X1_PARDE	Q3p7x1 paracoccus
28	33	76.7	720	Q582S8_9TRYP	Q582s8 trypanosoma
29	33	76.7	756	Q2UL42_ASPOR	Q2ul42 aspergillus
30	33	76.7	757	Q583B3_EMENI	Q583b3 aspergillus
31	33	76.7	777	Q9Z542_LYCES	Q9z542 lycopersico

32	76.7	811	2	Q89Z09_BACTN	Q89z09 bacteroides
33	76.7	904	2	Q6AIG9_DESPS	Q6aig9 desulfocale
34	76.7	1310	2	Q8A084_BACTN	Q8a084 bacteroides
35	76.7	16311	2	Q3AR72_CHLCH	Q3ar72 chlorobium
36	76.7	80	2	Q4XYD5_PLACH	Q4xyd5 plasmodium
37	76.7	147	2	Q93QN1_9ENTR	Q93qn1 brenneria s
38	76.7	147	2	Q93QN2_9ENTR	Q93qn2 brenneria s
39	76.7	147	2	Q93QN6_9ENTR	Q93qn6 brenneria s
40	76.7	150	2	Q4HSF7_CAMUP	Q4hsf7 campylobact
41	76.7	157	2	Q8D9U8_VIBUV	Q8d9u8 vibrio vuln
42	76.7	163	2	Q8CDH0_MOUSE	Q8cdh0 mus musculu
43	76.7	170	2	Q2IVR9_RHOPA	Q2ivr9 rhodopsendo
44	76.7	180	2	Q6N3U4_RHOPA	Q6n3u4 rhodopsendo
45	76.7	180	2	Q8XVY4_RALSO	Q8xvy4 ralsconia s

ALIGNMENTS

RESULT 1

Q2RSU4_RHURU PRELIMINARY; PRT; 350 AA.
ID Q2RSU4_RHURU PRELIMINARY; PRT; 350 AA.
AC Q2RSU4;
DT 24-JAN-2006, integrated into UniProtKB/TrEMBL.
DT 24-JAN-2006, sequence version 1.
DT 07-FEB-2006, entry version 2.
DE Hypothetical protein precursor.
GN ORFNames=Rru_A2001;
OS Rhodospirillum rubrum ATCC 11170.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
OC Rhodospirillaceae; Rhodospirillum.
OX NCBI_taxid=269796;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 11170;
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler J.C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Munk A.C., Brettin T., Bruce D.,
RA Han C., Tapia R., Gilna P., Schmutz J., Larimer F., Land M.,
RA Kyrpides N., Mavromatis K., Richardson P., Zhang Y., Roberts G.,
RA Reslewic S., Zhou S., Schwartz D.C.;
RT "Complete sequence of the chromosome of Rhodospirillum rubrum ATCC
11170".
RL Submitted (DEC-2005) to the EMBL/GenBank/DBJ databases.
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL; CP000230; ABC22801.1; -; Genomic_DNA.
DR Hypothetical protein; Signal.
KW SIGNAL
FT SIGNAL 1 26
SQ SEQUENCE 350 AA; 37513 MW; 5FB0C4570B989D7 CRC64;

Query Match 86.0%; Score 37; DB 2; Length 350;

Best Local Similarity 87.5%; Pred. No. 22;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SVSLSYRF 9

Db 343 SISLSYRF 350

RESULT 2

Q5MQD0_9CORO PRELIMINARY; PRT; 1356 AA.
ID Q5MQD0_9CORO PRELIMINARY; PRT; 1356 AA.
AC Q5MQD0;
DT 01-FEB-2005, integrated into UniProtKB/TrEMBL.
DT 01-FEB-2005, sequence version 1.
DT 21-FEB-2006, entry version 6.
DE Spike glycoprotein.
GN Name=S; ORFNames=HCV1gp3;
OS Human coronavirus HKU1
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus; Group 2 species;

```

OC unclassified Group 2 species.
OX NCBI_TaxID=290028;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HKU1;
RX PubMed=15613317; DOI=10.1128/JVI.79.2.894-895.2005;
RA Woo P.C., Lau S.K., Chu C.M., Chan K.H., Tsoi H.W., Huang Y.,
RA Wong B.H., Poon R.W., Cai J.J., Luk W.K., Poon L.L., Wong S.S.,
RA Guan Y., Peiris J.S., Yuen K.Y.;
RT "Characterization and complete genome sequence of a novel coronavirus,
RT coronavirus HKU1, from patients with pneumonia.";
RL J. Virol. 79:884-895(2005).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HKU1;
RA Woo P.C.Y., Lau S.K.P., Chan K.H., Tsoi H.W., Huang Y., Wong B.H.L.,
RA Cai J.J., Wong S.S.Y., Peiris J.S.M., Chu C.M., Yuen K.Y.;
RL Submitted (JAN-2006) to the EMBL/GenBank/DBJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AY597011; AAT98580.1; -; Genomic_RNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0006944; P:membrane fusion; IEA.
DR GO; GO:0046813; P:viral attachment, binding of host cell sur. .; IEA.
DR InterPro; IPR002552; Corona_S2.
DR Pfam; PF01601; Corona_S2; 1.
DR SEQUENCE 1356 AA; 151711 MW; EE319676930C844E CRC64;
SQ
Query Match 86.0%; Score 37; DB 2; Length 1356;
Best Local Similarity 77.8%; Pred. No. 99;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RSVSLSYRF 9
||:|||||
Db 760 RSISASYRF 768

RESULT 3
Q9LSL1 ARATH PRELIMINARY; PRT; 165 AA.
ID Q9LSL1;
AC Q9LSL1;
DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2000, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE Arabidopsis thaliana genomic DNA, chromosome 5, BAC clone F15L12.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Kaneko T., Katoh T., Asamizu E., Sato S., Nakamura Y., Kotani H.,
RA Tabata S.;
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AB026632; BAA97506.1; -; Genomic DNA.
SQ SEQUENCE 165 AA; 18500 MW; 8BBF132B3DDDD184 CRC64;

Query Match 81.4%; Score 35; DB 2; Length 165;
Best Local Similarity 87.5%; Pred. No. 26;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SVSLSYRF 9
|:|||||
Db 158 SLSLSYRF 165

```

```

RESULT 4
Q34VG2_9GAMM PRELIMINARY; PRT; 218 AA.
ID Q34VG2_9GAMM;
AC Q34VG2;
DT 06-DEC-2005, integrated into UniProtKB/TrEMBL.
DT 06-DEC-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Hypothetical protein precursor.
GN ORFNames=MgDRAFT_0253;
OS Alkalilimnicola ehrlichei MLHE-1.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Chromatiales;
OC Ectothiorhodospiraceae; Alkalilimnicola.
OX NCBI_TaxID=187272;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=MLHE-1;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RT "Sequencing of the draft genome and assembly of Alkalilimnicola
RT ehrlichei MLHE-1.";
RL Submitted (OCT-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=MLHE-1;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Laimer F., Land M.;
RT "Annotation of the draft genome of Alkalilimnicola ehrlichei MLHE-1.";
RL Submitted (NOV-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AALK0100027; EAP33167.1; -; Genomic_DNA.
DW Hypothetical protein; Signal.
FT SIGNAL 1 26 Potential.
SQ SEQUENCE 218 AA; 23556 MW; 739FCA2B0C70C1FE CRC64;

Query Match 81.4%; Score 35; DB 2; Length 218;
Best Local Similarity 87.5%; Pred. No. 36;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SVSLSYRF 9
||:|||||
Db 211 SVALSYRF 218

RESULT 5
Q5EGW8_9POXV PRELIMINARY; PRT; 322 AA.
ID Q5EGW8_9POXV;
AC Q5EGW8;
DT 15-MAR-2005, integrated into UniProtKB/TrEMBL.
DT 15-MAR-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE P32.
OS Goatpox virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Capripoxvirus.
OX NCBI_TaxID=186805;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Guo W.;
RT "Cloning and Expression of Capripoxvirus P32 Gene.";
RL Thesis (2004), Northeast Agriculture University, No.50, St. Mucai,
RL Harbin, Heilongjiang, People's Republic of China.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Guo W., Qu J., Xiang W., Li Y.;
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.

```



```

CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AY081707; AAW78648.1; -; mRNA.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR InterPro; IPR004900; Pox_P35.
DR Pfam; PF03213; Pox_P35; 1.
DR SEQUENCE 322 AA; 37559 MW; DC141BC26162CB7B CRC64;
Query Match 81.4%; Score 35; DB 2; Length 322;
Best Local Similarity 66.7%; Pred. No. 55;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 RVSLSYRF 9
DB 53 KDISLSYRF 61
RESULT 6
O23425 ARATH PRELIMINARY; PRT; 468 AA.
AC O23425;
DT 01-JAN-1998, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 29.
DE DNA chromosome 4, ESSA I CONTIG fragment NO. 4 (Hypothetical protein At4g15740).
GN Names:At4g15740; Synonyms:AT4g15740; OrderedLocusNames=At4g15740;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsiis.
OC NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Bevan M., Stiekema W., Murphy G., Wambutt R., Pohl T., Terry N.,
RA Kreis M., Stiekema W., Murphy G., Wambutt R., Pohl T., Terry N.,
RA Puigdomenech P., Hatzopoulos P., Obermaier B., Duesterhoft A.,
RA Jones J., Palme K., Ansorge W., Deiseny M., Bancroft I., Mewes H.W.,
RA Schueller C., Chaiwatiz N.;
RA Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA EU Arabidopsis sequencing project;
RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 2 C2 domains.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; Z97339; CAB10352.1; -; Genomic DNA.
DR EMBL; AL161542; CAB78616.1; -; Genomic DNA.
DR PIR; F71422; F71422.
DR TAIR; At4g15740; -.
DR InterPro; IPR000008; C2.
DR InterPro; IPR002052; N6_Mtase.
DR Pfam; PF00168; C2; 2.
DR SMART; SM00239; C2; 2.
DR PROSITE; PS50004; C2_DOMAIN; 1.
DR PROSITE; PS00092; N6_MTASE; UNKNOWN_1.
DR Hypothetical protein.
DR SEQUENCE 468 AA; 52292 MW; EF0035F3536D7877 CRC64;
Query Match 81.4%; Score 35; DB 2; Length 468;
Best Local Similarity 87.5%; Pred. No. 84;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 SVLSYRF 9
DB 174 TVLSYRF 181

```

```

RESULT 7
Q5LDZ9 BACFN PRELIMINARY; PRT; 1125 AA.
AC Q5LDZ9;
DT 21-JUN-2005, integrated into UniProtKB/TrEMBL.
DT 21-JUN-2005, sequence version 1.
DT 07-FEB-2006, entry version 9.
DE Putative outer membrane protein.
GN OrderedLocusNames=BF1956;
OS Bacteroides fragilis (strain ATCC 25285 / NCTC 9343).
OC Bacteria; Bacteroidetes; Bacteroidetes (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OC NCBI_TaxID=272559;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA Cerdeno-Tarraga A.-M., Patrick S., Crossman L.C., Blakely G.,
RA Abratt V., Lennard N., Poxton I., Duerden B., Harris B., Quail M.A.,
RA Barron A., Clark L., Corton C., Doggett J., Holden M.T.G., Larke N.,
RA Line A., Lord A., Norbertczak H., Ormond D., Price C.,
RA Rabinowitsch E., Woodward J., Barrell B.G., Parkhill J.;
RA "Extensive DNA inversions in the B. fragilis genome control variable
RT gene expression.";
RL Science 307:1463-1465(2005).
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; CR626927; CAH07654.1; -; Genomic DNA.
DR GO; GO:0019867; C:outer membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR Complete proteome; Membrane; Outer membrane; TonB box.
DR SEQUENCE 1125 AA; 124651 MW; 05A9F2D5D67856C3 CRC64;
Query Match 81.4%; Score 35; DB 2; Length 1125;
Best Local Similarity 66.7%; Pred. No. 2.2e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 RVSLSYRF 9
DB 1051 REITLSYRF 1059
RESULT 8
Q93TH9 BACFR PRELIMINARY; PRT; 1125 AA.
AC Q93TH9;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 26.
DE Outer membrane protein Omp121.
GN OrderedLocusNames=BF1894;
OS Bacteroides fragilis.
OC Bacteria; Bacteroidetes; Bacteroidetes (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OC NCBI_TaxID=817;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC25285;
RX MEDLINE=21856486; PubMed=11867216; DOI=10.1016/S0378-1119(01)00835-6;
RA Wexler H.M., Read E.K., Tomaszynski T.J.;
RA "Characterization of omp200, a porin gene complex from Bacteroides
RT fragilis: omp121 and omp71, gene sequence, deduced amino acid
RT sequences and predictions of porin structure.";
RL Gene 283:95-105(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=YCH46;
RX PubMed=15466707; DOI=10.1073/pnas.0404172101;
RA Kuwahara T., Yamashita A., Hirakawa H., Nakayama H., Toh H., Okada N.,
RA Kuhara S., Hattori M., Hayashi T., Ohnishi Y.;

```

RT "Genomic analysis of Bacteroides fragilis reveals extensive DNA
 RT inversions regulating cell surface adaptation."
 RL Proc. Natl. Acad. Sci. U.S.A. 101:14919-14924(2004).
 CC -----

CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----

DR EMBL; AF357210; AAK38604.1; -; Genomic DNA.
 DR EMBL; AP006841; BAD48642.1; -; Genomic DNA.
 DR GO; GO:00019867; C:outer membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0005215; F:transporter activity; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR012910; Plug.
 DR InterPro; IPR000531; TonB_dep_rcpt.
 DR Pfam; PF07715; Plug; 1.
 DR Pfam; PF00593; TonB_dep_Rec; 1.
 KW Complete proteome; Membrane; Outer membrane; TonB box.
 SQ SEQUENCE 1125 AA; 124651 MW; 05A9P2D5D67856C3 CRC64;

Query Match 81.4%; Score 35; DB 2; Length 1125;
 Best Local Similarity 66.7%; Pred. No. 2.2e+02; Mismatches 1; Indels 0; Gaps 0;
 Matches 6; Conservative 2;

Qy 1 RSVLSYRF 9

Db 1051 REITLSYRF 1059

RESULT 9

ID Q3G2T8_9DELTA PRELIMINARY; PRT; 333 AA.
 AC Q3G2T8_9DELTA
 DT 08-NOV-2005, integrated into UniProtKB/TrEMBL.
 DT 07-FEB-2006, entry version 1.
 DE Hypothetical protein precursor.
 OS Pelobacter propionicus DSM 2379.
 GN ORFNames=ProBRAFT 1321;
 GN Pelobacter propionicus DSM 2379.
 OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
 OC Pelobacteraceae; Pelobacter.
 OX NCBI_TaxID=338966;
 RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=DSM 2379;
 RG US DOE Joint Genome Institute (JGI-PGF);
 RA Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T.,
 RA Hammon N., Israni S., Pitluck S., Richardson P.;
 RT "Sequencing of the draft genome and assembly of Pelobacter propionicus
 RT DSM 2379."
 RL Submitted (AUG-2005) to the EMBL/GenBank/DBSJ databases.
 RN [2]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=DSM 2379;
 RG US DOE Joint Genome Institute (JGI-ORNL);
 RA Larimer F., Land M.;
 RT "Annotation of the draft genome assembly of Pelobacter propionicus DSM
 RT 2379."
 RL Submitted (AUG-2005) to the EMBL/GenBank/DBSJ databases.
 CC !- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBSJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC -----

CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----

DR EMBL; AAJH01000010; EAO36301.1; -; Genomic DNA.

KW Hypothetical protein; Signal.
 FT SIGNAL 1 37 Potential.

SQ SEQUENCE 333 AA; 37659 MW; B90D457D78EA5109 CRC64;

Query Match 79.1%; Score 34; DB 2; Length 333;
 Best Local Similarity 87.5%; Pred. No. 96;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 2 SVLSYRF 9
 Db 326 SVSLEYRF 333

RESULT 10

Q6D6D4_ERWCT PRELIMINARY; PRT; 366 AA.
 ID Q6D6D4_ERWCT
 AC Q6D6D4;
 DT 16-AUG-2004, integrated into UniProtKB/TrEMBL.
 DT 16-AUG-2004, sequence version 1.
 DT 07-FEB-2006, entry version 10.
 DE Outer-membrane protein A.
 GN Name=ompA; OrderedLocustNames=ECA1751;
 OS Erwinia carotovora subsp. atroseptica (Pectobacterium atrosepticum).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Pectobacterium.
 OX NCBI_TaxID=29471;

RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=SCRI 1043 / ATCC BAA-672;
 RX PubMed=15263089; DOI=10.1073/pnas.0402424101;
 RA Bell K.S., Sebahia M., Pritchard L., Holden M.T.G., Hyman L.J.,
 RA Holvea M.C., Thomson N.R., Bentley S.D., Churcher L.J.C., Mungall K.,
 RA Atkin R., Bason N., Brooks K., Chillingworth T., Clark K., Doggett J.,
 RA Fraser A., Hance Z., Hauser H., Jagels K., Moule S., Norbertczak H.,
 RA Ormond D., Price C., Quail M.A., Sanders M., Walker D., Whitehead S.,
 RA Salmund G.P.C., Birch P.R.J., Parkhill J., Toth I.K.;
 RT "Genome sequence of the enterobacterial phytopathogen Erwinia
 RT carotovora subsp. atroseptica and characterization of virulence
 RT factors."
 RL Proc. Natl. Acad. Sci. U.S.A. 101:11105-11110(2004).

CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----

EMBL; BX950851; CAG74656.1; -; Genomic DNA.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0009279; C:outer membrane (sensu Gram-negative Bacteria); IEA.

DR GO; GO:0005198; F:structural molecule activity; IEA.

DR InterPro; IPR006664; Bac_OmpA.

DR InterPro; IPR002368; OmpA.

DR InterPro; IPR006665; OmpA/MotB.

DR InterPro; IPR006690; OMPA_LIKE.

DR InterPro; IPR000498; OmpA_TM.

DR Pfam; PF00691; OmpA; 1.

DR PRINTS; PR01389; OmpA_membrane; 1.

DR PRINTS; PR01021; OMPADOMAIN.

DR PRODOM; PD000930; OmpA/MotB; 1.

DR PROSITE; PS01068; OMPA_1; 1.

KW Complete proteome.

SQ SEQUENCE 366 AA; 39013 MW; 7BD65E03C6179F25 CRC64;

Query Match 79.1%; Score 34; DB 2; Length 366;

Best Local Similarity 87.5%; Pred. No. 1.1e+02; Mismatches 1; Indels 0; Gaps 0;
 Matches 7; Conservative 0;

Qy 2 SVLSYRF 9

Db 201 SVGLSYRF 208

RESULT 11

Q9RM69_ERWCA PRELIMINARY; PRT; 367 AA.
 ID Q9RM69_ERWCA
 AC Q9RM69;
 DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
 DT 01-MAY-2000, sequence version 1.
 DT 07-FEB-2006, entry version 20.

DE Putative outer-membrane protein A precursor.

GN Name=ompA;
OS Erwinia carotovora.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Pectobacterium.
OX NCBI_TaxID=554;
[1]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=MFC10;
RA El-hamel C., Chevalier S., De E., Orange N., Molle G.;
RT "Isolation and characterization of the major outer membrane protein of
RT Erwinia carotovora MFC10.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL; AJ249340; CAB57308.1; -; Genomic_DNA.
DR HSSP; P02934; 1QJP.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0009279; C: outer membrane (sensu Gram-negative Bacteria); IEA.
DR GO; GO:0005198; F: structural molecule activity; IEA.
DR InterPro; IPR006664; Bac_OmpA.
DR InterPro; IPR002368; OmpA.
DR InterPro; IPR006665; OmpA/MotB.
DR InterPro; IPR000498; OmpA_TM.
DR Pfam; PF00691; OmpA; 1.
DR Pfam; PF01389; OmpA_membrane; 1.
DR PRINTS; PR01021; OMPADOMAIN.
DR PRINTS; PR01022; OUTRMBRANEA.
DR ProDom; PD000930; OmpA/MotB; 1.
KW Signal.
FT SIGNAL
FT CHAIN
FT CHAIN 22 367 potential outer-membrane protein A.
SQ SEQUENCE 367 AA; 39293 MW; 04F74B421F3DEFB7 CRC64;
Query Match 79.1%; Score 34; DB 2; Length 367;
Best Local Similarity 87.5%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 2 SVLSYRPF 9
DB 196 SVGLSYRPF 203

RESULT 12
Q4BP04_BURVI PRELIMINARY; PRT; 372 AA.
ID Q4BP04_BURVI
AC Q4BP04;
DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 13-SEP-2005, sequence version 1.
DT 07-FEB-2006, entry version 2.
DE Hypothetical protein.
GN ORFNames=Bcep1808DRAFT_6246;
OS Burkholderia vietnamiensis G4.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.
OX NCBI_TaxID=269482;
[1]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=G4;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RT "Sequencing of the draft genome and assembly of Burkholderia
RT vietnamiensis G4.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL; U60646; AAB49273.1; -; Genomic_DNA.
DR HSSP; P02934; 1G90.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0009279; C: outer membrane (sensu Gram-negative Bacteria); IEA.
DR GO; GO:0005198; F: structural molecule activity; IEA.
DR InterPro; IPR006664; Bac_OmpA.

RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
[3]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=G4;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RA Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL; AABH0200006; EAM31978.1; -; Genomic_DNA.
DR Hypothetical protein.
SQ SEQUENCE 372 AA; 42840 MW; 2254A94030D5D138 CRC64;
Query Match 79.1%; Score 34; DB 2; Length 372;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
OY 1 RVSLSYRPF 9
DB 68 RATSISYRPF 76

RESULT 13
P96773_HAEDU PRELIMINARY; PRT; 403 AA.
ID P96773_HAEDU
AC P96773; Q7BY82;
DT 01-MAY-1997, integrated into UniProtKB/TrEMBL.
DT 01-MAY-1997, sequence version 1.
DT 07-FEB-2006, entry version 28.
DE Major outer membrane protein.
GN Name=ompA; Synonyms=nomp; OrderedLocusNames=HD0045; ORFNames=HD_0045;
OS Haemophilus ducreyi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=730;
[1]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=35000;
RX MEDLINE=97197543; PubMed=9045839;
RA Kleenev-Tait J.A., Hiltke T.J., Maciver I., Spinola S.M., Radolf J.D.,
RA Hansen E.J.;
RT "The major outer membrane protein of Haemophilus ducreyi consists of
RT two ompA homologs.";
RL J. Bacteriol. 179:1764-1773 (1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=35000;
RA Kleenev-Tait J.A., Hiltke T., Spinola S., Ralldolf J., Hansen E.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=35000HP / ATCC 700724;
RA Munson R.S. Jr., Ray W.C., Mahairas G., Sabo P., Mungur R.,
RA Johnson L., Nguyen D., Wang J., Forst C., Hood L.;
RT "The complete genome sequence of Haemophilus ducreyi.";
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL; U60646; AAB49273.1; -; Genomic_DNA.
DR HSSP; P02934; 1G90.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0009279; C: outer membrane (sensu Gram-negative Bacteria); IEA.
DR GO; GO:0005198; F: structural molecule activity; IEA.
DR InterPro; IPR006664; Bac_OmpA.

```
DR InterPro; IPR002368; OmpA.
DR InterPro; IPR006665; OmpA/MotB.
DR InterPro; IPR000498; OmpA_TM.
DR Pfam; PF00691; OmpA; 1.
DR Pfam; PF01389; OmpA_membrane; 1.
DR PRINTS; PR01021; OMPADOMAIN.
DR PRINTS; PR01022; OTRMBRANEA.
DR ProDom; PD000930; OmpA/MotB; 1.
KW Complete proteome.
SQ SEQUENCE 403 AA; 44172 MW; 44292568EB37736C CRC64;

Query Match 79.1%; Score 34; DB 2; Length 403;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 SVSLSYRF 9
DB 247 SVGLSYRF 254

RESULT 14
Q2S253 9SPHI PRELIMINARY; PRT; 433 AA.
AC Q2S253;
DT 24-JAN-2006, integrated into UniProtKB/TrEMBL.
DT 24-JAN-2006, sequence version 1.
DT 07-MAR-2006, entry version 3.
DE DnaJ domain protein.
GN ORFNames=SRU_1607;
OS Salinibacter ruber DSM 13855.
OC Bacteria; Bacteroidetes; Sphingobacteriales;
OC Crenotrichaceae; Salinibacter.
OX NCBI_TaxID=309807;
RN [1]_TaxID=309807;
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DSM 13855;
RX PubMed=16330755; DOI=10.1073/pnas.0509073102;
RA Mongodin E.F., Nelson K.E., Daugherty S., Deboy R.T., Wister J.,
RA Khouri H., Weidman J., Waleh D.A., Papke R.T., Sanchez Perez G.,
RA Sharma A.K., Nesbo C.L., Macleod D., Baptiste E., Doolittle W.F.,
RA Charlebois R.L., Legault B., Rodriguez-Valera F.;
RT "The genome of Salinibacter ruber: Convergence and gene exchange among
hyperhalophilic bacteria and archaea.";
RL Proc. Natl. Acad. Sci. U.S.A. 102:18147-18152(2005).
CC -!- SUBCELLULAR LOCATION: Membrane-bound. Mitochondrial; inner
CC membrane (By similarity).
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; CP000159; ABC4394.1; -; Genomic DNA.
KW Chapterone; Inner membrane; Membrane; Protein transport; Translocation;
KW Transmembrane; Transport.
KW SEQUENCE 433 AA; 48388 MW; 6E8C151D56CB50E1 CRC64;

Query Match 79.1%; Score 34; DB 2; Length 433;
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSVLSYR 8
DB 185 RSVLSLYR 192

RESULT 15
Q9DQ91 9CLOS PRELIMINARY; PRT; 559 AA.
AC Q9DQ91;
DT 01-MAR-2001, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2001, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE RNA-dependent RNA polymerase (fragment).
OS Pineapple mealybug wilt-associated virus 2.
```

```
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Closteroviridae;
OC Ampelovirus.
OX NCBI_TaxID=136234;
RN [1]_TaxID=136234;
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21064595; PubMed=11125151;
RA Melzer M.J., Karasev A.V., Sether D.M., Hu J.S.;
RT "Nucleotide sequence, genome organization and phylogenetic analysis of
RT pineapple mealybug wilt-associated virus-2.";
RL J. Gen. Virol. 82:1-7(2001).
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AF283103; AAG13939.1; -; Genomic DNA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR GO; GO:0019079; P:viral genome replication; IEA.
DR InterPro; IPR001788; RNA_dep_RNAPol2.
DR InterPro; IPR007095; RNA_pol_DS_PS.
DR InterPro; IPR007094; RNA_pol_PSVir.
DR Pfam; PF00978; RdRP_2; 1.
KW RNA-directed RNA polymerase.
FT NON_TER 1
SQ SEQUENCE 559 AA; 64784 MW; 6736F4972E264DD2 CRC64;

Query Match 79.1%; Score 34; DB 2; Length 559;
Best Local Similarity 87.5%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 SVSLSYRF 9
DB 53 SVSLDYRF 60

Search completed: August 10, 2006, 23:09:58
Job time : 153 secs
```

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 10, 2006, 23:01:01 ; Search time 12.3636 Seconds
(without alignments)
46.693 Million cell updates/sec

Title: US-10-825-603-3

Perfect score: 28

Sequence: 1 VLSYSR 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 80: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	100.0	89	IS3416	interleukin-8 homo
2	28	100.0	89	A53497	pre-B-cell growth-
3	28	100.0	93	G01540	cytokine SDF-1-bet
4	28	100.0	93	I81182	cytokine - mouse
5	28	100.0	172	T10891	hemolysin-coregula
6	28	100.0	218	B81150	bacteriocin resist
7	28	100.0	218	H81871	probable periplasm
8	28	100.0	380	T29875	hypothetical prote
9	28	100.0	435	A11017	probable type-I se
10	28	100.0	439	T14872	ABC exporter outer
11	28	100.0	468	F71422	hypothetical prote
12	28	100.0	596	ACRYE	acetylcholinestera
13	28	100.0	599	A38868	acetylcholinestera
14	28	100.0	1017	D90550	vsaa-like (mycopla
15	27	96.4	1500	T03824	probable immediate
16	27	96.4	1513	T44045	hypothetical prote
17	27	96.4	1520	T44231	hypothetical prote
18	26	92.9	160	H88114	protein F53C3.6 [i
19	26	92.9	348	B44509	aldose 1-epimerase
20	26	92.9	682	B70121	hypothetical prote
21	26	92.9	860	F86349	hypothetical prote
22	25	89.3	135	B80258	hypothetical phage
23	25	89.3	169	B84033	VPS29-like phospho
24	25	89.3	172	B90658	hypothetical prote
25	25	89.3	172	C85509	hypothetical prote
26	25	89.3	172	AD0451	conserved hypothet
27	25	89.3	194	A10489	conserved hypothet
28	25	89.3	196	G82622	conserved hypothet
29	25	89.3	203	G95309	conserved hypothet

30	25	89.3	212	2	AB3611	hypothetical prote
31	25	89.3	212	2	H97392	mca/sah nucleosida
32	25	89.3	213	2	A86654	hypothetical prote
33	25	89.3	218	2	G75281	conserved hypothet
34	25	89.3	245	2	F71887	hypothetical prote
35	25	89.3	287	2	AD3412	aminomethyltransfe
36	25	89.3	302	2	S76323	hypothetical prote
37	25	89.3	305	2	T17117	protein kinase cdc
38	25	89.3	395	1	MMCWTF	major outer membra
39	25	89.3	402	2	E75370	hypothetical prote
40	25	89.3	406	2	G97185	membrane protein o
41	25	89.3	410	2	H86290	hypothetical prote
42	25	89.3	420	2	E70914	probable lipo prot
43	25	89.3	482	2	AD3142	transcription regu
44	25	89.3	482	2	H98145	transcription regu
45	25	89.3	540	2	A75250	carboxylesterase,

ALIGNMENTS

RESULT 1

IS3416

interleukin-8 homolog - mouse

C:Species: Mus sp. (mouse)

C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999

C:Accession: IS3416

R:Jiang, W.; Zhou, P.; Kahn, S.M.; Tomita, N.; Johnson, M.D.; Weinstein, I.B.

Exp. Cell Res. 215, 284-293, 1994

A>Title: Molecular cloning of TPARI, a gene whose expression is repressed by the tumor

A:Reference number: IS3416; MUID:95073497; PMID:7982471

A:Accession: IS3416

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-89 <RES>

A:Cross-references: UNIPARC:UPI00000018A3; GB:S74318; NID:G786393; PIDN:AAB32650.1; PID

C:Genetics:

A:Gene: TPARI

C:Superfamily: beta-thromboglobulin

Query Match 100.0%; Score 28; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLSYSR 6
|||
Db 24 VLSYSR 29

RESULT 2

A53497

pre-B-cell growth-stimulating factor precursor - mouse

C:Species: Mus musculus (house mouse)

C>Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 09-Jul-2004

C:Accession: A53497; I59582

R:Nagasawa, T.; Kikutani, H.; Kishimoto, T.

Proc. Natl. Acad. Sci. U.S.A. 91, 2305-2309, 1994

A>Title: Molecular cloning and structure of a pre-B-cell growth-stimulating factor.

A:Reference number: A53497; MUID:94181581; PMID:8134392

A:Accession: A53497

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-89 <NAG>

A:Cross-references: UNIPROT:P40224; UNIPARC:UPI00000018A3; GB:D21072; NID:G413905; PIDN

R:Tashiro, K.; Tada, H.; Heilker, R.; Shirozu, M.; Nakano, T.; Honjo, T.

Science 261, 600-603, 1993

A>Title: Signal sequence trap: a cloning strategy for secreted proteins and type I mem

A:Reference number: I59582; MUID:93342488; PMID:8342023

A:Accession: I59582

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-89 <RES>

A:Cross-references: UNIPARC:UPI00000018A3; GB:I12029; NID:G393179; PIDN:AAA40100.1; PID

C:Genetics:

A:Gene: SDF-1-alpha
A:Superfamily: beta-thromboglobulin
C:Keywords: cytokine

Query Match 100.0%; Score 28; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLSLYR 6
|||||
DB 24 VLSLYR 29

RESULT 3

G01540

Cytokine SDF-1-beta - human
C:Species: Homo sapiens (man)

C>Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004

C:Accession: G01540

R:Spotila, L.D.

submitted to the EMBL Data Library, October 1994

A:Reference number: G07697

A:Accession: G01540

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-93 <SPO>

A:Cross-references: UNIPROT:P48061; UNIPARC:UPI000003092F; EMBL:U16752; NID:g1272194; PI

C:Superfamily: beta-thromboglobulin

Query Match 100.0%; Score 28; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLSLYR 6
|||||
DB 24 VLSLYR 29

RESULT 4

I81182

cytokine - mouse

C:Species: Mus musculus (house mouse)

C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004

C:Accession: I81182

R:Tashiro, K.; Tada, H.; Heilker, R.; Shirozu, M.; Nakano, T.; Honjo, T.

Science 261, 600-603, 1993

A:Title: Signal sequence trap: a cloning strategy for secreted proteins and type I memb

A:Reference number: 159582; MUID:93342488; PMID:8342023

A:Accession: I81182

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-93 <RES>

A:Cross-references: UNIPROT:P40224; UNIPARC:UPI000002A125; GB:L12030; NID:g393181; PIDN:

C:Genetics:

A:Gene: SDF-1-beta

C:Superfamily: beta-thromboglobulin

Query Match 100.0%; Score 28; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLSLYR 6
|||||
DB 24 VLSLYR 29

RESULT 5

T10891

hemolysin-coregulated protein Hcp VC1415 VCA0017 [similarity] - Vibrio cholerae (strain

C:Species: Vibrio cholerae

C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004

C:Accession: T10891; C82202; E82511

R:Williams, S.G.; Varcoe, L.T.; Attridge, S.R.; Manning, P.A.

Infect. Immun. 64, 283-289, 1996

A:Title: Vibrio cholerae Hcp, a secreted protein coregulated with HlyA.

A:Reference number: Z17200; MUID:96110945; PMID:8557353

A:Accession: T10891

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-172 <WIL>

A:Cross-references: UNIPROT:P72350; UNIPARC:UPI00000D40CC; EMBL:S81006; NID:g1488370; PI

R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;

chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.

1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000

A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A:Reference number: A82035; MUID:20406833; PMID:10952301

A:Accession: C82202

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-172 <HEI>

A:Cross-references: UNIPARC:UPI00000D40CC; GB:AE004220; GB:AE003852; NID:g9655910; PIDN:

A:Experimental source: serogroup O1; strain N16961; biotype El Tor

A:Accession: E82511

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-172 <HE2>

A:Cross-references: UNIPARC:UPI00000D40CC; GB:AE004345; GB:AE003853; NID:g9657390; PIDN:

A:Experimental source: serogroup O1; strain N16961; biotype El Tor

C:Genetics: <GEN1>

A:Gene: hcpB

A:Note: the hcpA and hcpB proteins are identical

C:Genetics: <GEN2>

A:Gene: VC1415

A:Map position: 1

C:Genetics: <GEN3>

A:Gene: VCA0017

A:Map position: 2

C:Superfamily: Vibrio cholerae hemolysin-coregulated protein

Query Match 100.0%; Score 28; DB 2; Length 172;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLSLYR 6
|||||
DB 144 VLSLYR 149

RESULT 6

B81150

bacteriocin resistance protein, probable NMB0855 [imported] - Neisseria meningitidis (st

C:Species: Neisseria meningitidis

C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004

A:Accession: B81150

R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.

Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;

ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M.

Science 287, 1809-1815, 2000

A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve

A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.

A:Reference number: A81000; MUID:20175755; PMID:10710307

A:Accession: B81150

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-218 <TET>

A:Cross-references: UNIPROT:Q9JZX8; UNIPARC:UPI00000C45AB; GB:AE002439; GB:AE002098; NID:

A:Experimental source: serogroup B, strain MC58

C:Genetics:

A:Gene: NMB0855

Query Match 100.0%; Score 28; DB 2; Length 218;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLSYSR 6
 |||||
 Db 15 VLSYSR 20

RESULT 7
 H81871
 probable periplasmic protein NMA1066 [imported] - Neisseria meningitidis (strain Z2491 s
 C:Species: Neisseria meningitidis
 C>Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
 C:Accession: H81871
 R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
 ; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
 Nature 404, 502-506, 2000
 A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
 A:Reference number: A81775; MUID:20222556; PMID:10761919
 A:Accession: H81871
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-218 <PAR>
 A:CROSS-references: UNIPROT:Q9JUZ8; UNIPARC:UPI000000C4AED; GB:AL1162755; GB:AL1157959; NID
 A:Experimental source: serogroup A, strain Z2491
 C:Genetics:
 A:Gene: NMA1066

Query Match 100.0%; Score 28; DB 2; Length 218;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLSYSR 6
 |||||
 Db 15 VLSYSR 20

RESULT 8
 T29875
 hypothetical protein F32B5.2 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Dec-2004
 C:Accession: T29875
 R:Bedwith, J.; Graves, T.; Biewald, T.
 submitted to the EMBL Data Library, May 1997
 A:Description: The sequence of C. elegans cosmid F32B5.
 A:Reference number: Z20702
 A:Accession: T29875
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-380 <LED>
 A:CROSS-references: UNIPROT:O01853; UNIPARC:UPI00000783FE; EMBL:AF003148; PIDN:AAB54207.
 A:Experimental source: strain Bristol N2; clone F32B5
 C:Genetics:
 A:Gene: CESP:F32B5.2
 A:Map position: 1
 A:Introns: 47/3; 99/2; 195/3; 227/1; 264/2; 333/3

Query Match 100.0%; Score 28; DB 2; Length 380;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLSYSR 6
 |||||
 Db 288 VLSYSR 293

RESULT 9
 A11017
 probable type-I secretion protein STY4456 [imported] - Salmonella enterica subsp. enteri
 C:Species: Salmonella enterica subsp. enterica serovar typhi
 A:Note: this species has also been called Salmonella typhi
 C>Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
 C:Accession: A11017
 R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
 th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,

S.; Moule, S.; O'Gaora, P.
 Nature 413, 848-852, 2001
 A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K
 A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica sero
 A:Reference number: AB0502; MUID:21534947; PMID:11677608
 A:Accession: A11017
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-435 <PAR>
 A:CROSS-references: UNIPARC:UPI000005A847; GB:AL513382; PIDN:CAD09242.1; PID:g16505246;
 C:Genetics:
 A:Gene: STY4456

Query Match 100.0%; Score 28; DB 2; Length 435;
 Best Local Similarity 100.0%; Pred. No. 41;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLSYSR 6
 |||||
 Db 90 VLSYSR 95

RESULT 10
 T14872
 ABC exporter outer membrane component homolog - Salmonella typhimurium
 C:Species: Salmonella typhimurium
 C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
 C:Accession: T14872
 R;Wong, K.K.; McClelland, M.; Stillwell, L.C.; Sisk, E.C.; Thurston, S.J.; Saffer, J.D
 Infect. Immun. 66, 3365-3371, 1998
 A:Title: Identification and sequence analysis of a 27-kilobase chromosomal fragment con
 oar typhimurium LT2.
 A:Reference number: Z18249; MUID:98298059; PMID:9632606
 A:Accession: T14872
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-439 <WON>
 A:CROSS-references: UNIPROT:O85313; UNIPARC:UPI000000B3B2A; EMBL:AF060869; NID:g33232584;
 C:Genetics:
 A:Gene: spi4_C
 A:Map position: 92 min

Query Match 100.0%; Score 28; DB 2; Length 439;
 Best Local Similarity 100.0%; Pred. No. 41;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLSYSR 6
 |||||
 Db 90 VLSYSR 95

RESULT 11
 F71422
 hypothetical protein - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 A:Variety: Columbia
 C>Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 09-Jul-2004
 C:Accession: F71422
 R;Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dir
 P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzenecker, T.; Pohl, T.M.; Tarryn, N.; Gie
 avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B.
 Nature 391, 485-488, 1998
 A:Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenech
 erhoft, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; An
 C.; Chalwatzis, N.
 A:Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis tha
 A:Reference number: A71400; MUID:98121113; PMID:9461215
 A:Accession: F71422
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-468 <BEV>
 A:CROSS-references: UNIPROT:O23425; UNIPARC:UPI00000A66FB; GB:Z97339; NID:g2244901; PID
 C:Genetics:

A;Map position: 4COP9-4G3845

Query Match 100.0%; Score 28; DB 2; Length 468;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLSYR 6
|||||
DB 175 VLSYR 180

RESULT 12

ACRYE

acetylcholinesterase (EC 3.1.1.7) precursor, l1s form [validated] - Pacific electric ray
N;Alternate names: acetylcholinesterase, asymmetric form
C;Species: Torpedo californica (Pacific electric ray)

C;Date: 17-Mar-1987 #sequence revision 08-Nov-1996 #text change 09-Jul-2004
C;Accession: A00773; A60820; A31962; B31962; A2302; B4117; S15677
R;Schumacher, M.; Camp, S.; Maulet, Y.; Newton, M.; MacPhee-Quigley, K.; Taylor, S.S.; R
Nature 319, 407-409, 1986

A;Title: Primary structure of Torpedo californica acetylcholinesterase deduced from its
A;Reference number: A00773; MUID:86118676; PMID:3753747

A;Accession: A00773
A;Molecule type: mRNA

A;Residues: 'NS',11-596 <SCH>
A;Cross-references: UNIPROT:P04058; UNIPARC:UPI000017279D; GB:X03439; NID:G64389

A;Experimental source: electric organ
A;Note: parts of this sequence, including the amino and carboxyl ends of the mature prod

R;Schumacher, M.; Camp, S.; Maulet, Y.; Newton, M.; MacPhee-Quigley, K.; Taylor, S.S.; R
Fed. Proc. 45, 2976-2981, 1986

A;Title: Primary structure of acetylcholinesterase: implications for regulation and func
A;Reference number: A60820; MUID:87054662; PMID:3536598

A;Accession: A60820
A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA
A;Residues: 22-596 <SC2>

A;Cross-references: UNIPARC:UPI00001471B0
R;Schumacher, M.; Maulet, Y.; Camp, S.; Taylor, P.

J. Biol. Chem. 263, 18979-18987, 1988
A;Title: Multiple messenger RNA species give rise to the structural diversity in acetyl

A;Reference number: A92701; MUID:89066695; PMID:3198606
A;Accession: A31962

A;Molecule type: mRNA
A;Residues: 1-23 <SC3>

A;Cross-references: UNIPARC:UPI000017279E; EMBL:X03439; NID:G64389
A;Experimental source: clones ACHB-11 and ACHB-18

A;Note: revision to sequence A00773
A;Accession: B31962

A;Molecule type: DNA; mRNA
A;Residues: 499-565 <SC4>

A;Cross-references: UNIPARC:UPI000017279F; GB:X03439; NID:G64389
A;Experimental source: clone ACHB-1

R;MacPhee-Quigley, K.; Taylor, P.; Taylor, S.
J. Biol. Chem. 260, 12185-12189, 1985

A;Title: Primary structures of the catalytic subunits from two molecular forms of acetyl
A;Reference number: A23902; MUID:86008285; PMID:3900071

A;Accession: A23902
A;Molecule type: protein

A;Residues: 22,'B',24-45;214-237 <MAC>
A;Cross-references: UNIPARC:UPI00001727A0; UNIPARC:UPI00001727A1

A;Note: active site Ser identification
R;Kreienkamp, H.J.; Weise, C.; Raba, R.; Aaviksaar, A.; Hucho, F.

Proc. Natl. Acad. Sci. U.S.A. 88, 6117-6121, 1991
A;Title: Anionic subsites of the catalytic center of acetylcholinesterase from Torpedo a

A;Reference number: A4117; MUID:91296772; PMID:2068091
A;Accession: B4117

A;Molecule type: protein
A;Residues: 100-108 <KRE>

A;Cross-references: UNIPARC:UPI00001727A2
A;Note: substrate binding site

R;Maulet, Y.; Camp, S.; Gibney, G.; Rachinsky, T.L.; Ekstroem, T.J.; Taylor, P.
Neuron 4, 289-301, 1990

A;Title: Single gene encodes glycopospholipid-anchored and asymmetric acetylcholinester

A;Reference number: P80113; MUID:90166618; PMID:2306366

A;Accession: S15677

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 557-596 <MAU>

A;Cross-references: UNIPARC:UPI00001727A3; EMBL:X56516

R;MacPhee-Quigley, K.; Vedvick, T.S.; Taylor, P.; Taylor, S.S.

J. Biol. Chem. 261, 13565-13570, 1986

A;Title: Profile of the disulfide bonds in acetylcholinesterase.

A;Reference number: A43099; MUID:87008586; PMID:3759980

A;Contents: annotation; disulfide bonds

R;Suesman, J.L.; Harel, M.; Silman, I.

submitted to the Brookhaven Protein Data Bank, October 1991

A;Reference number: A50061; PDB:1ACE

A;Contents: annotation; X-ray crystallography, 2.8 angstroms, residues 26-481,511-555 of

R;Suesman, J.L.; Harel, M.; Frolow, F.; Oefner, C.; Goldman, A.; Tokar, L.; Silman, I.

Science 253, 872-879, 1991

A;Title: Atomic structure of acetylcholinesterase from Torpedo californica: a prototypic

A;Reference number: A43098; MUID:91343928; PMID:1678899

A;Contents: annotation; X-ray crystallography, 2.8 angstroms, residues 26-481,511-555 of

C;Comment: Synapses usually contain this l1s (asymmetric) form of cholinesterase with a

holinesterase occurs on the outer surfaces of cell membranes, including those of erythro

C;Complex: l1s form is disulfide linked homodimer; l8s form is homotetramer, a dimer of

C;Function:

A;Description: hydrolyzes acetylcholine to choline and acetate

A;Pathway: neurotransmitter degradation

C;Superfamily: cholinesterase; cholinesterase homology

C;Keywords: alternative splicing; carboxylic ester hydrolase; glycoprotein; membrane pro

F;1-21/Domain: signal sequence #status predicted <SIG>

F;22-596/Product: acetylcholinesterase, l1s form #status experimental <MAT>

F;51-551/Domain: cholinesterase homology <CHE>

F;80-478,554/Binding site: carbohydrate (Asn) (covalent) #status predicted

F;88-115,275-286,423-542/Disulfide bonds: #status experimental

F;105/Binding site: substrate (Trp) #status experimental

F;221/Active site: Ser #status experimental

F;348,461/Active site: Glu, His #status predicted

F;437/Binding site: carbohydrate (Asn) (covalent) #status experimental

F;593/Disulfide bonds: interchain #status experimental

Query Match 100.0%; Score 28; DB 1; Length 596;

Best Local Similarity 100.0%; Pred. No. 56;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLSYR 6

|||||

DB 165 VLSYR 170

RESULT 13

A38868

acetylcholinesterase (EC 3.1.1.7) precursor - marbled electric ray

C;Species: Torpedo marmorata (marbled electric ray)

C;Date: 23-Apr-1993 #sequence revision 15-Nov-1996 #text_change 09-Jul-2004

C;Accession: A38868; A29682; S15696; A25650

R;Massoulié, J.; Bon, S.

submitted to the EMBL Data Library, June 1992

A;Reference number: A38868

A;Accession: A38868

A;Molecule type: mRNA

A;Residues: 1-599 <MAS>

A;Cross-references: UNIPROT:P07692; UNIPARC:UPI000002A334; EMBL:X05497;

R;Sikorav, J.L.; Krejci, E.; Massoulié, J.

EMBO J. 6, 1865-1873, 1987

A;Title: cDNA sequences of Torpedo marmorata acetylcholinesterase: primary structure of

A;Reference number: A29682; MUID:86004392; PMID:2820709

A;Accession: A29682

A;Molecule type: mRNA

A;Residues: 1-40,'G',42-226,'G',274-284,'E',286-420,'N',422-599 <STK>

A;Cross-references: UNIPARC:UPI00001727A4; EMBL:X05497

R;Sikorav, J.L.; Duval, N.; Anselmet, A.; Bon, S.; Krejci, E.; Legay, C.; Osterlund, M.,

EMBO J. 7, 2983-2993, 1988

A;Title: Complex alternative splicing of acetylcholinesterase transcripts in Torpedo elc

A;Reference number: S01293; MUID:89030590; PMID:3181125

A;Accession: S15696
 A;Molecule type: mRNA
 A;Residues: 526-599 <SI2>
 A;Cross-references: UNIPARC:UPI00001714C5; EMBL:X13172; NID:g64416; PIDN:CAA31570.1; PID
 A;Experimental source: clone pACh2
 R;Bon, S.; Chang, J.Y.; Strosberg, A.D.
 FEBS Lett. 209, 206-212, 1986
 A;Title: Identical N-terminal peptide sequences of asymmetric forms and of low-salt-solu
 inesterase.
 A;Reference number: A91370; MUID:87080761; PMID:3792544
 A;Accession: A25650
 A;Molecule type: protein
 A;Residues: 25-40, 'G', 42-47 <BON>
 A;Cross-references: UNIPARC:UPI00001727A5
 C;Genetics:
 A;Gene: AChE

C;Function:
 A;Description: hydrolyzes acetylcholine to choline and acetate
 A;Pathway: neurotransmitter degradation
 C;Superfamily: cholinesterase; cholinesterase homology
 C;Keywords: alternative splicing; carboxylic ester hydrolase; glycoprotein; neurotransmi
 F;1-24/Domain: signal sequence #status predicted <SIG>
 F;25-599/Product: acetylcholinesterase #status predicted <MAT>
 F;54-554/Domain: cholinesterase homology <CHE>
 F;83,440,481,557/Binding site: carboxylate (Asn) (covalent) #status predicted
 F;91-118,278-289,426-545/Disulfide bonds: #status predicted
 F;224,351,464/Active site: Ser, Glu, His #status predicted
 F;596/Disulfide bonds: interchain #status predicted

Query Match 100.0%; Score 28; DB 1; Length 599;
 Best Local Similarity 100.0%; Pred. No. 56;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLSYR 6
 |||||
 Db 168 VLSYR 173

RESULT 14

D90550
 vsaa-like (mycoplasma pulmonis) protein [imported] - Mycoplasma pulmonis (strain UAB CTI
 C;Species: Mycoplasma pulmonis
 C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
 C;Accession: D90550
 R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
 Nucleic Acids Res. 29, 2145-2153, 2001
 A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm
 A;Reference number: A99512; MUID:21267165; PMID:11353084
 A;Accession: D90550
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-1017 <KUR>
 A;Cross-references: UNIPROT:Q98QQ3; UNIPARC:UPI0000045B6; GB:AL445566; PID:g14089722; F
 A;Experimental source: strain UAB CTIP
 C;Genetics:
 A;Gene: MYPU_3080
 A;Genetic code: SGC3

Query Match 100.0%; Score 28; DB 2; Length 1017;
 Best Local Similarity 100.0%; Pred. No. 97;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLSYR 6
 |||||
 Db 219 VLSYR 224

RESULT 15

T03824
 probable immediate early protein 2 - human herpesvirus 6
 C;Species: human herpesvirus 6
 C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
 C;Accession: T03824

R;Soergel, A.; Schiewe, U.; Fleckenstein, B.; Neipel, F.
 submitted to the EMBL Data Library, July 1997
 A;Description: Identification of an human herpesvirus-6 transcription unit homologous t
 A;Reference number: Z15104
 A;Accession: T03824

A;Status: preliminary; translated from GB/EMBL/DBDJ
 A;Molecule type: mRNA
 A;Residues: 1-1500 <SOE>
 A;Cross-references: UNIPROT:O42080; UNIPARC:UPI000000F1CS2; EMBL:AF015297; NID:g23433282;
 C;Genetics:
 A;Gene: iezhom

Query Match 96.4%; Score 27; DB 2; Length 1500;
 Best Local Similarity 83.3%; Pred. No. 2.6e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLSYR 6
 :|||
 Db 377 ISLSYR 382

Search completed: August 10, 2006, 23:11:10
 Job time : 13.3636 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 10, 2006, 23:10:21 ; Search time 32.1818 Seconds
(without alignments)
24.479 Million cell updates/sec

Title: US-10-825-603-1

Perfect score: 43

Sequence: 1 RVSLSYRF 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /EMC_Celerra_SID33/ptodata/2/iaa/5 COMB.pep.*
- 2: /EMC_Celerra_SID33/ptodata/2/iaa/6 COMB.pep.*
- 3: /EMC_Celerra_SID33/ptodata/2/iaa/7 COMB.pep.*
- 4: /EMC_Celerra_SID33/ptodata/2/iaa/H COMB.pep.*
- 5: /EMC_Celerra_SID33/ptodata/2/iaa/PCTUS COMB.pep.*
- 6: /EMC_Celerra_SID33/ptodata/2/iaa/RE COMB.pep.*
- 7: /EMC_Celerra_SID33/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	81.4	55	2	US-09-270-767-39075
2	35	81.4	55	2	US-09-270-767-54292
3	32	74.4	70	2	US-09-248-796A-23114
4	32	74.4	396	2	US-10-094-749-2492
5	32	74.4	445	2	US-10-104-047-2209
6	32	74.4	859	2	US-09-708-200-7
7	32	74.4	859	2	US-09-788-657-16
8	32	74.4	859	2	US-09-712-691-5
9	32	74.4	859	2	US-09-707-468C-5
10	32	74.4	859	2	US-10-641-068-16
11	32	74.4	859	2	US-09-760-285-14
12	31	72.1	336	2	US-09-902-540-11471
13	31	72.1	406	2	US-09-543-681A-4268
14	31	72.1	708	2	US-09-252-991A-23303
15	30	69.8	9	2	US-09-646-193-2
16	30	69.8	9	2	US-09-646-193-3
17	30	69.8	9	2	US-09-646-192-2
18	30	69.8	9	2	US-09-646-192-3
19	30	69.8	10	2	US-09-646-193-4
20	30	69.8	10	2	US-09-646-192-4
21	30	69.8	86	2	US-09-252-991A-20089
22	30	69.8	90	2	US-09-134-001C-5426
23	30	69.8	250	2	US-09-270-767-35537
24	30	69.8	250	2	US-09-270-767-50754
25	30	69.8	262	2	US-09-252-991A-25231
26	30	69.8	268	2	US-09-252-991A-30879

27	30	69.8	360	2	US-09-489-039A-13055	Sequence 13055, A
28	30	69.8	364	2	US-09-418-980-8	Sequence 8, Appli
29	30	69.8	364	2	US-09-809-665A-151	Sequence 151, App
30	30	69.8	364	2	US-09-506-078-45	Sequence 45, Appl
31	30	69.8	438	1	US-08-282-197C-59	Sequence 59, Appl
32	30	69.8	567	2	US-10-172-527A-7	Sequence 7, Appli
33	30	69.8	567	3	US-11-120-422-7	Sequence 7, Appli
34	30	69.8	568	2	US-09-469-200E-10	Sequence 10, Appl
35	30	69.8	568	2	US-10-011-768B-10	Sequence 10, Appl
36	30	69.8	588	5	PCT-US95-13749-4	Sequence 4, Appli
37	30	69.8	712	1	US-08-121-713D-64	Sequence 64, Appl
38	30	69.8	712	1	US-08-835-268-64	Sequence 64, Appl
39	30	69.8	712	1	US-09-060-692-64	Sequence 64, Appl
40	30	69.8	712	2	US-08-833-391-64	Sequence 64, Appl
41	30	69.8	712	2	US-09-060-610-64	Sequence 64, Appl
42	30	69.8	712	5	PCT-US94-10151A-64	Sequence 64, Appl
43	30	69.8	1426	2	US-09-136-574A-43	Sequence 43, Appl
44	29	67.4	8	2	US-09-430-470-18	Sequence 18, Appl
45	29	67.4	12	2	US-09-132-521-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-09-270-767-39075
; Sequence 39075, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 39075
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-39075

Query Match 81.4%; Score 35; DB 2; Length 55;
Best Local Similarity 87.5%; Pred. No. 3.2;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	2	SVSLSYRF	9
DB	15	SLSLSYRF	22

RESULT 2

US-09-270-767-54292
; Sequence 54292, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 54292
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-54292

Query Match 81.4%; Score 35; DB 2; Length 55;
Best Local Similarity 87.5%; Pred. No. 3.2;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
QY      2 SVSLSYRF 9
Db      15 SLSLSYRF 22

RESULT 3
US-09-248-796A-23114
; Sequence 23114, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 23114
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-23114

Query Match      74.4%; Score 32; DB 2; Length 70;
Best Local Similarity 55.6%; Pred. No. 18;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1 RSVLSYRF 9
Db      46 RDIALNYRF 54

RESULT 4
US-10-094-749-2492
; Sequence 2492, Application US/10094749
; Patent No. 6979557
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHKO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOUYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
; FILE REFERENCE: 084335/0160
; CURRENT APPLICATION NUMBER: US/10/094,749
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/350,435
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: JP 2001-328381
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 3381
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2492
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Homo sapiens
```

```
US-10-094-749-2492

Query Match      74.4%; Score 32; DB 2; Length 396;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 RSVLSYRF 9
Db      188 RPSVSTYRF 196

RESULT 5
US-10-104-047-2209
; Sequence 2209, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: NO. 6943241el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2209
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-2209

Query Match      74.4%; Score 32; DB 2; Length 445;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 RSVLSYRF 9
Db      237 RPSVSTYRF 245

RESULT 6
US-09-708-200-7
; Sequence 7, Application US/09708200
; Patent No. 6576468
; GENERAL INFORMATION:
; APPLICANT: Nicolaides, Nicholas C
; APPLICANT: Grasso, Luigi
; APPLICANT: SASS, Philip M
; TITLE OF INVENTION: METHODS FOR ISOLATING NOVEL ANTIMICROBIAL AGENTS FROM
; FILE OF INVENTION: HYPERMUTABLE CELLS
; FILE REFERENCE: MOR-0005
; CURRENT APPLICATION NUMBER: US/09/708,200
; CURRENT FILING DATE: 2000-11-07
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 859
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-708-200-7

Query Match      74.4%; Score 32; DB 2; Length 859;
Best Local Similarity 77.8%; Pred. No. 2.8e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 RSVLSYRF 9
Db      301 RSLSLMRF 309

RESULT 7
US-09-788-657-16
; Sequence 16, Application US/09788657
```

```
; Patent No. 6656736
; GENERAL INFORMATION:
; APPLICANT: Nicolaides, Nicholas
; APPLICANT: Sass, Philip
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Grasso, Luigi
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Methods for generating hypermutable
; FILE REFERENCE: 01107.00097
; CURRENT APPLICATION NUMBER: US/09/788,657
; CURRENT FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 60/184,336
; PRIOR FILING DATE: 2000-02-23
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 859
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-788-657-16

Query Match      74.4%; Score 32; DB 2; Length 859;
Best Local Similarity 77.8%; Pred. No. 2.8e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 RSVLSLYRF 9
Db      301 RSLSLSMRF 309

RESULT 8
US-09-712-691-5
; Sequence 5, Application US/09712691
; Patent No. 6737268
; GENERAL INFORMATION:
; APPLICANT: Nicolaides, Nicholas C
; APPLICANT: Grasso, Luigi M
; APPLICANT: Sass, Philip M
; TITLE OF INVENTION: METHODS FOR GENERATING GENETICALLY ALTERED ANTIGENS
; FILE REFERENCE: MOR-0015
; CURRENT APPLICATION NUMBER: US/09/712,691
; CURRENT FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 859
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-712-691-5

Query Match      74.4%; Score 32; DB 2; Length 859;
Best Local Similarity 77.8%; Pred. No. 2.8e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 RSVLSLYRF 9
Db      301 RSLSLSMRF 309

RESULT 9
US-09-707-468C-5
; Sequence 5, Application US/09707468C
; Patent No. 6808894
; GENERAL INFORMATION:
; APPLICANT: Nicolaides, Nicholas C
; APPLICANT: Grasso, Luigi
; APPLICANT: Sass, Philip M
; TITLE OF INVENTION: Methods For Generating Genetically Altered Antibody-Producing
; TITLE OF INVENTION: Cell Lines With Improved Antibody Characteristics
; FILE REFERENCE: MOR-0003
; CURRENT APPLICATION NUMBER: US/09/707,468C
; CURRENT FILING DATE: 2000-11-07
```

```
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 859
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-707-468C-5

Query Match      74.4%; Score 32; DB 2; Length 859;
Best Local Similarity 77.8%; Pred. No. 2.8e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 RSVLSLYRF 9
Db      301 RSLSLSMRF 309

RESULT 10
US-10-641-068-16
; Sequence 16, Application US/10641068
; Patent No. 6921666
; GENERAL INFORMATION:
; APPLICANT: Nicolaides, Nicholas
; APPLICANT: Sass, Philip
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Grasso, Luigi
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Methods for generating hypermutable
; FILE REFERENCE: 01107.00097
; CURRENT APPLICATION NUMBER: US/10/641,068
; CURRENT FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: US/09/788,657
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 60/184,336
; PRIOR FILING DATE: 2000-02-23
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 859
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-641-068-16

Query Match      74.4%; Score 32; DB 2; Length 859;
Best Local Similarity 77.8%; Pred. No. 2.8e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 RSVLSLYRF 9
Db      301 RSLSLSMRF 309

RESULT 11
US-09-760-285-14
; Sequence 14, Application US/09760285
; Patent No. 6982169
; GENERAL INFORMATION:
; APPLICANT: Nicolaides, Nicholas C
; APPLICANT: Grasso, Luigi
; APPLICANT: Sass, Philip M
; TITLE OF INVENTION: CHEMICAL INHIBITORS OF MISMATCH REPAIR
; FILE REFERENCE: MOR-0017
; CURRENT APPLICATION NUMBER: US/09/760,285
; CURRENT FILING DATE: 2001-01-15
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 859
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-760-285-14
```

```
Query Match      74.4%; Score 32; DB 2; Length 859;
Best Local Similarity 77.8%; Pred. No. 2.8e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 RVSLSYRF 9
DB      301 RSLSLMRF 309

RESULT 12
US-09-902-540-11471
; Sequence 11471, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 11471
; LENGTH: 336
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-11471

Query Match      72.1%; Score 31; DB 2; Length 336;
Best Local Similarity 75.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 RVSLSYRF 8
DB      35 RAVSLNRF 42

RESULT 13
US-09-543-681A-4268
; Sequence 4268, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 4268
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-4268

Query Match      72.1%; Score 31; DB 2; Length 406;
Best Local Similarity 66.7%; Pred. No. 2e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 RVSLSYRF 9
DB      206 RGLPLSYRF 214

RESULT 14
US-09-252-991A-25303
; Sequence 25303, Application US/09252991A
; Patent No. 6551795
```

```
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 25303
; LENGTH: 708
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25303

Query Match      72.1%; Score 31; DB 2; Length 708;
Best Local Similarity 85.7%; Pred. No. 3.7e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      3 VLSYRF 9
DB      530 LSLSYRF 536

RESULT 15
US-09-646-193-2
; Sequence 2, Application US/09646193
; Patent No. 6875738
; GENERAL INFORMATION:
; APPLICANT: Clark-Lewis, Ian
; APPLICANT: Duronio, Vincent
; APPLICANT: Salari, Hassan
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: Therapeutic Chemokine Receptor Antagonists
; FILE REFERENCE: 080353-000000US
; CURRENT APPLICATION NUMBER: US/09/646,193
; CURRENT FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: CA 2,245,224
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: WO PCT/CA99/00221
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: WO PCT/CA99/00750
; PRIOR FILING DATE: 1999-08-16
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CXCR4
; OTHER INFORMATION: antagonist peptide compound N-terminal sequence
; NAME/KEY: MOD_RES
; LOCATION: (9)-
; OTHER INFORMATION: Xaa = Cys or Cys modified by a polypeptide
; OTHER INFORMATION: homologous to a portion of SDF-1
US-09-646-193-2

Query Match      69.8%; Score 10; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 5e+05;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 RVSLSYRF 8
DB      1 KGVLSYRF 8

Search completed: August 10, 2006, 23:13:11
Job time : 32.1818 secs
```


THIS PAGE BLANK (USPTO)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 10, 2006, 23:10:21 ; Search time 21.4545 Seconds
(without alignments)
24.479 Million cell updates/sec

Title: US-10-825-603-3

Perfect score: 28

Sequence: 1 VLSYR 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5 COMB.pep.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6 COMB.pep.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7 COMB.pep.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H COMB.pep.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/iaa/pCTUS COMB.pep.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE COMB.pep.*
- 7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	100.0	8	2	US-09-430-470-18
2	28	100.0	9	2	US-09-646-193-2
3	28	100.0	9	2	US-09-646-193-3
4	28	100.0	9	2	US-09-646-192-2
5	28	100.0	9	2	US-09-646-192-3
6	28	100.0	10	2	US-09-646-193-4
7	28	100.0	10	2	US-09-646-192-4
8	28	100.0	12	2	US-09-132-521-2
9	28	100.0	14	2	US-09-543-940-10
10	28	100.0	17	2	US-09-646-193-1
11	28	100.0	17	2	US-09-646-192-1
12	28	100.0	31	2	US-09-543-940-5
13	28	100.0	32	2	US-09-144-838-12
14	28	100.0	32	2	US-09-144-838-14
15	28	100.0	33	2	US-09-144-838-11
16	28	100.0	33	2	US-09-144-838-13
17	28	100.0	66	2	US-09-144-838-27
18	28	100.0	66	2	US-09-144-838-29
19	28	100.0	66	2	US-09-144-838-35
20	28	100.0	66	2	US-09-144-838-37
21	28	100.0	67	2	US-09-144-838-8
22	28	100.0	67	2	US-09-144-838-23
23	28	100.0	67	2	US-09-144-838-25
24	28	100.0	67	2	US-09-144-838-28
25	28	100.0	67	2	US-09-144-838-30
26	28	100.0	67	2	US-09-144-838-31

27	28	100.0	67	2	US-09-144-838-33	Sequence 33, Appl
28	28	100.0	67	2	US-09-144-838-36	Sequence 36, Appl
29	28	100.0	67	2	US-09-144-838-38	Sequence 38, Appl
30	28	100.0	67	2	US-09-646-193-6	Sequence 6, Appli
31	28	100.0	67	2	US-09-646-192-6	Sequence 6, Appli
32	28	100.0	68	2	US-09-144-838-24	Sequence 24, Appl
33	28	100.0	68	2	US-09-144-838-26	Sequence 26, Appl
34	28	100.0	68	2	US-09-144-838-32	Sequence 32, Appl
35	28	100.0	68	2	US-09-144-838-34	Sequence 34, Appl
36	28	100.0	68	2	US-09-175-713-14	Sequence 14, Appl
37	28	100.0	69	2	US-09-175-713-10	Sequence 10, Appl
38	28	100.0	72	2	US-09-175-713-15	Sequence 15, Appl
39	28	100.0	72	2	US-09-646-193-7	Sequence 7, Appli
40	28	100.0	72	2	US-09-646-192-7	Sequence 7, Appli
41	28	100.0	73	2	US-09-175-713-11	Sequence 11, Appl
42	28	100.0	81	2	US-09-248-796A-24270	Sequence 24270, A
43	28	100.0	89	1	US-08-181-556-2	Sequence 2, Appli
44	28	100.0	89	1	US-08-323-084A-1	Sequence 1, Appli
45	28	100.0	89	1	US-08-674-008-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-430-470-18
; Sequence 18, Application US/09430470
; Patent No. 6562800
; GENERAL INFORMATION:
; APPLICANT: McMillan, Minnie
; TITLE OF INVENTION: THE USE OF IMMUNOPOTENTIATING SEQUENCES
; FILE REFERENCE: 13761-725
; CURRENT APPLICATION NUMBER: US/09/430,470
; CURRENT FILING DATE: 1999-10-29
; EARLIER APPLICATION NUMBER: US 60/106,506
; EARLIER FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-430-470-18

Query Match	100.0%	Score 28;	DB 2;	Length 8;
Best Local Similarity	100.0%	Pred. No. 5e+05;	0;	Indels 0;
Matches	6;	Conservative	0;	Mismatches 0;
QY	1	VLSYR 6		
Db	3	VLSYR 8		
RESULT 2				
US-09-646-193-2				
; Sequence 2, Application US/09646193				
; Patent No. 6875738				
; GENERAL INFORMATION:				
; APPLICANT: Clark-Lewis, Ian				
; APPLICANT: Duronio, Vincent				
; APPLICANT: Salari, Hassan				
; APPLICANT: The University of British Columbia				
; TITLE OF INVENTION: Therapeutic Chemokine Receptor Antagonists				
; FILE REFERENCE: 080353-000000US				
; CURRENT APPLICATION NUMBER: US/09/646,193				
; CURRENT FILING DATE: 2000-09-13				
; PRIOR APPLICATION NUMBER: CA 2,245,224				
; PRIOR FILING DATE: 1998-08-14				
; PRIOR APPLICATION NUMBER: WO PCT/CA99/00221				
; PRIOR FILING DATE: 1999-03-12				
; PRIOR APPLICATION NUMBER: WO PCT/CA99/00750				
; PRIOR FILING DATE: 1999-08-16				

```
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CXCR4
; OTHER INFORMATION: antagonist peptide compound N-terminal sequence
; NAME/KEY: MOD_RES
; LOCATION: (9)
; OTHER INFORMATION: Xaa = Cys or Cys modified by a polypeptide
; OTHER INFORMATION: homologous to a portion of SDF-1
US-09-646-193-2

Query Match          100.0%; Score 28; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLSYR 6
Db 3 VLSYR 8

RESULT 3
US-09-646-193-3
; Sequence 3, Application US/09646193
; Patent No. 6875738
; GENERAL INFORMATION:
; APPLICANT: Clark-Lewis, Ian
; APPLICANT: Duronio, Vincent
; APPLICANT: Salari, Hassan
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: Therapeutic Chemokine Receptor Antagonists
; FILE REFERENCE: 080353-000000US
; CURRENT APPLICATION NUMBER: US/09/646,193
; CURRENT FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: CA 2,245,224
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: WO PCT/CA99/00221
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CXCR4
; OTHER INFORMATION: antagonist peptide compound of dimerized
; OTHER INFORMATION: N-terminal amino acid sequence SDF-1(1-8)-2
; NAME/KEY: MOD_RES
; LOCATION: (9)
; OTHER INFORMATION: Xaa = any brige forming moiety, such as ornithine or
; OTHER INFORMATION: L-amino-N-butyric acid in which two amino groups are used to form
; OTHER INFORMATION: linkage between dimerized SDF-1(1-8)-2, or Lys, where the epsilon
; OTHER INFORMATION: amino group forms an amide bond to Arg in the peptide
; OTHER INFORMATION: Arg-Tyr-Ser-Leu-Ser-Val-Gly-Lys, represented from the carboxyl to
; OTHER INFORMATION: amino end
US-09-646-193-3

Query Match          100.0%; Score 28; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLSYR 6
Db 3 VLSYR 8
```

```
RESULT 4
US-09-646-192-2
; Sequence 2, Application US/09646192
; Patent No. 6946445
; GENERAL INFORMATION:
; APPLICANT: Clark-Lewis, Ian
; APPLICANT: Gong, Jiang-Hong
; APPLICANT: Duronio, Vincent
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: Therapeutic Chemokine Receptor Antagonists
; FILE REFERENCE: 080352-000000US
; CURRENT APPLICATION NUMBER: US/09/646,192
; CURRENT FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: CA 2,226,391
; PRIOR FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: CA 2,245,224
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: WO PCT/CA99/00221
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CXCR4
; OTHER INFORMATION: antagonist peptide compound N-terminal sequence
; NAME/KEY: MOD_RES
; LOCATION: (9)
; OTHER INFORMATION: Xaa = Cys or Cys modified by a polypeptide
; OTHER INFORMATION: homologous to a portion of SDF-1
US-09-646-192-2

Query Match          100.0%; Score 28; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLSYR 6
Db 3 VLSYR 8

RESULT 5
US-09-646-192-3
; Sequence 3, Application US/09646192
; Patent No. 6946445
; GENERAL INFORMATION:
; APPLICANT: Clark-Lewis, Ian
; APPLICANT: Gong, Jiang-Hong
; APPLICANT: Duronio, Vincent
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: Therapeutic Chemokine Receptor Antagonists
; FILE REFERENCE: 080352-000000US
; CURRENT APPLICATION NUMBER: US/09/646,192
; CURRENT FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: CA 2,226,391
; PRIOR FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: CA 2,245,224
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: WO PCT/CA99/00221
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CXCR4
; OTHER INFORMATION: antagonist peptide compound of dimerized
```

```

; NAME/KEY: MOD RES
; LOCATION: (9)
; OTHER INFORMATION: Xaa = Lys, where the epsilon amino group forms an
; OTHER INFORMATION: amide bond to Arg in the peptide
; OTHER INFORMATION: Arg-Tyr-Ser-Leu-Ser-Val-Gly-Lys, represented from
; OTHER INFORMATION: the carboxyl to amino end
US-09-646-192-3

Query Match          100.0%; Score 28; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLSYR 6
Db 3 VLSYR 8

RESULT 6
US-09-646-193-4
; Sequence 4, Application US/09646193
; Patent No. 6875738
; GENERAL INFORMATION:
; APPLICANT: Clark-Lewis, Ian
; APPLICANT: Duronio, Vincent
; APPLICANT: Salari, Hasan
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: Therapeutic Chemokine Receptor Antagonists
; FILE REFERENCE: 080353-000000US
; CURRENT APPLICATION NUMBER: US/09/646,193
; CURRENT FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: CA 2,245,224
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: WO PCT/CA99/00221
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: WO PCT/CA99/00750
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CXCR4
; OTHER INFORMATION: antagonist peptide compound of dimerized
; OTHER INFORMATION: N-terminal amino acid sequence SDF-1(1-9)-2
; NAME/KEY: MOD RES
; LOCATION: (10)
; OTHER INFORMATION: Xaa = any bridge forming moiety, such as ornithine or
; OTHER INFORMATION: L-amino-N-butyric acid in which two amino groups are used to form
; OTHER INFORMATION: linkage between dimerized SDF-1(1-9)-2, or Lys, where the epsilon
; OTHER INFORMATION: amino group forms an amide bond to Arg in the peptide
; OTHER INFORMATION: Cys-Arg-Ser-Leu-Ser-Val-Gly-Lys, represented from the carboxyl to
; OTHER INFORMATION: amino end
US-09-646-193-4

Query Match          100.0%; Score 28; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLSYR 6
Db 3 VLSYR 8

RESULT 7
US-09-646-192-4
; Sequence 4, Application US/09646192
; Patent No. 6946445
; GENERAL INFORMATION:
; APPLICANT: Clark-Lewis, Ian
; APPLICANT: Gong, Jiang-Hong

```

```

; APPLICANT: Duronio, Vincent
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: Therapeutic Chemokine Receptor Antagonists
; FILE REFERENCE: 080352-000000US
; CURRENT APPLICATION NUMBER: US/09/646,192
; CURRENT FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: CA 2,226,391
; PRIOR FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: CA 2,245,224
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: WO PCT/CA99/00221
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CXCR4
; OTHER INFORMATION: antagonist peptide compound of dimerized
; OTHER INFORMATION: N-terminal amino acid sequence
; NAME/KEY: MOD RES
; LOCATION: (10)
; OTHER INFORMATION: Xaa = Lys, where the epsilon amino group forms an
; OTHER INFORMATION: amide bond to Cys in the peptide
; OTHER INFORMATION: Cys-Arg-Ser-Leu-Ser-Val-Gly-Lys, represented from
; OTHER INFORMATION: the carboxyl to amino end
US-09-646-192-4

Query Match          100.0%; Score 28; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLSYR 6
Db 3 VLSYR 8

RESULT 8
US-09-132-521-2
; Sequence 2, Application US/09132521
; Patent No. 6828138
; GENERAL INFORMATION:
; APPLICANT: Nagai, Yoshiyuki
; APPLICANT: Shioda, Tatsuo
; APPLICANT: Moriya, Chikaya
; TITLE OF INVENTION: Recombinant sendai virus vector
; TITLE OF INVENTION: comprising a gene encoding chemokine
; FILE REFERENCE: 50026/008001
; CURRENT APPLICATION NUMBER: US/09/132,521
; CURRENT FILING DATE: 1998-08-11
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 9, 11
; OTHER INFORMATION: Xaa is predicted to be Cys
US-09-132-521-2

Query Match          100.0%; Score 28; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLSYR 6
Db 3 VLSYR 8

```

```
RESULT 9
US-09-543-940-10
; Sequence 10, Application US/09543940
; Patent No. 6613742
; GENERAL INFORMATION:
; APPLICANT: Huang, Ziwei
; APPLICANT: Luo, Zhaowen
; APPLICANT: Zhou, Naiming
; APPLICANT: Luo, Jiansong
; TITLE OF INVENTION: Chemokine-Derived Synthetic Peptides
; FILE REFERENCE: 8321-40
; CURRENT APPLICATION NUMBER: US/09/543,940
; CURRENT FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/128,106
; PRIOR FILING DATE: 1999-04-07
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide containing segment from N-terminal region
; OTHER INFORMATION: of human SDF-1 protein
US-09-543-940-10

Query Match      100.0%; Score 28; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VLSYR 6
Db      3 VLSYR 8

RESULT 10
US-09-646-193-1
; Sequence 1, Application US/09646193
; Patent No. 6875738
; GENERAL INFORMATION:
; APPLICANT: Clark-Lewis, Ian
; APPLICANT: Duronio, Vincent
; APPLICANT: Salari, Haasan
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: Therapeutic Chemokine Receptor Antagonists
; FILE REFERENCE: 080353-000000US
; CURRENT APPLICATION NUMBER: US/09/646,193
; CURRENT FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: CA 2,245,224
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: WO PCT/CA99/00221
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: WO PCT/CA99/00750
; PRIOR FILING DATE: 1999-08-16
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:two putative
; OTHER INFORMATION: CXCR4 binding sites joined by the CXC motif
US-09-646-193-1

Query Match      100.0%; Score 28; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VLSYR 6
Db      3 VLSYR 8

RESULT 11
US-09-646-192-1
; Sequence 1, Application US/09646192
; Patent No. 6946445
; GENERAL INFORMATION:
; APPLICANT: Clark-Lewis, Ian
; APPLICANT: Gong, Jiang-Hong
; APPLICANT: Duronio, Vincent
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: Therapeutic Chemokine Receptor Antagonists
; FILE REFERENCE: 080352-000000US
; CURRENT APPLICATION NUMBER: US/09/646,192
; CURRENT FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: CA 2,226,391
; PRIOR FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: CA 2,245,224
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: WO PCT/CA99/00221
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:two putative
; OTHER INFORMATION: CXCR4 binding sites joined by the CXC motif
US-09-646-192-1

Query Match      100.0%; Score 28; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VLSYR 6
Db      3 VLSYR 8

RESULT 12
US-09-543-940-5
; Sequence 5, Application US/09543940
; Patent No. 6613742
; GENERAL INFORMATION:
; APPLICANT: Huang, Ziwei
; APPLICANT: Luo, Zhaowen
; APPLICANT: Zhou, Naiming
; APPLICANT: Luo, Jiansong
; TITLE OF INVENTION: Chemokine-Derived Synthetic Peptides
; FILE REFERENCE: 8321-40
; CURRENT APPLICATION NUMBER: US/09/543,940
; CURRENT FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/128,106
; PRIOR FILING DATE: 1999-04-07
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide containing segments from N- and C-terminal
; OTHER INFORMATION: regions of human SDF-1 protein
US-09-543-940-5

Query Match      100.0%; Score 28; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VLSYR 6
```

```
Db          3 VLSYR 8
|||||
US-09-144-838-12
; Sequence 12, Application US/09144838A
; Patent No. 6844161
; GENERAL INFORMATION:
; APPLICANT: Siani, Michael A.
; APPLICANT: Wilken, Jill
; APPLICANT: Simon, Reyna
; APPLICANT: Kent, Stephen B.H.
; TITLE OF INVENTION: Modular Protein Libraries and Methods of Preparation
; FILE REFERENCE: GRFN-020/01US
; CURRENT APPLICATION NUMBER: US/09/144,838A
; EARLIER FILING DATE: 1998-08-31
; EARLIER FILING DATE: 1997-09-04
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-144-838-11
; Sequence 11, Application US/09144838A
; Patent No. 6844161
; GENERAL INFORMATION:
; APPLICANT: Siani, Michael A.
; APPLICANT: Wilken, Jill
; APPLICANT: Simon, Reyna
; APPLICANT: Kent, Stephen B.H.
; TITLE OF INVENTION: Modular Protein Libraries and Methods of Preparation
; FILE REFERENCE: GRFN-020/01US
; CURRENT APPLICATION NUMBER: US/09/144,838A
; EARLIER FILING DATE: 1998-08-31
; EARLIER FILING DATE: 1997-09-04
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-144-838-11
Query Match          100.0%; Score 28; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 VLSYR 6
           |||||
Db          3 VLSYR 8

Search completed: August 10, 2006, 23:13:12
Job time : 22.4545 secs
```

RESULT 15

THIS PAGE BLANK (USPTO)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 10, 2006, 22:52:41 ; Search time 80.1818 Seconds
(without alignments)
34.213 Million cell updates/sec

Title: US-10-825-603-3

Perfect score: 28

Sequence: 1 VLSYR 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq 8:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*
9: Geneseq2005s:*
10: Geneseq2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	100.0	6	ADU18132	Adu18132 Immune ce
2	28	100.0	8	AAY34090	Aay34090 CXCR4 ant
3	28	100.0	8	AAY67591	Aay67591 SDF-1 N-t
4	28	100.0	8	AAB47684	Aab47684 SDF-1(1-8
5	28	100.0	8	ADA50222	Ada50222 Mouse SDF
6	28	100.0	9	AAY34089	Aay34089 CXCR4 ant
7	28	100.0	9	AAY67590	Aay67590 SDF-1 N-t
8	28	100.0	9	AAY67592	Aay67592 SDF-1 pep
9	28	100.0	9	AAB47711	Aab47711 SDF-1(1-9
10	28	100.0	9	AAB47682	Aab47682 SDF-1(1-9
11	28	100.0	9	AAM48662	Aam48662 CXCR4 pep
12	28	100.0	9	ADU18130	Adu18130 Immune ce
13	28	100.0	9	ADU18131	Adu18131 Immune ce
14	28	100.0	9	ADU18134	Adu18134 Immune ce
15	28	100.0	11	AAY08416	Aay08416 CXCR-4 re
16	28	100.0	11	AAY086006	Aay086006 Modified
17	28	100.0	11	ADR51445	Adr51445 Dipeptidyl
18	28	100.0	12	AAY08417	Aay08417 CXCR-4 re
19	28	100.0	12	AAY91089	Aay91089 Human SDF
20	28	100.0	12	ADV67125	Adv67125 Human SDF
21	28	100.0	13	AAY08430	Aay08430 CXCR-4 re
22	28	100.0	13	AAY08429	Aay08429 CXCR-4 re
23	28	100.0	13	AAY08420	Aay08420 CXCR-4 re

24	28	100.0	13	2	AAY08437	Aay08437 CXCR-4 re
25	28	100.0	13	2	AAY08432	Aay08432 CXCR-4 re
26	28	100.0	13	2	AAY08435	Aay08435 CXCR-4 re
27	28	100.0	13	2	AAY08436	Aay08436 CXCR-4 re
28	28	100.0	13	2	AAY08431	Aay08431 CXCR-4 re
29	28	100.0	13	2	AAY08428	Aay08428 CXCR-4 re
30	28	100.0	14	2	AAY08425	Aay08425 CXCR-4 re
31	28	100.0	14	2	AAY08424	Aay08424 CXCR-4 re
32	28	100.0	14	3	AAB28550	Aab28550 Chemokine
33	28	100.0	15	2	AAY08427	Aay08427 CXCR-4 re
34	28	100.0	16	6	ABP55613	Abp55613 Human cyt
35	28	100.0	17	2	AAY34088	Aay34088 Stromal c
36	28	100.0	17	3	AAY67589	Aay67589 SDF-1 put
37	28	100.0	17	5	AAB47712	Aab47712 SDF-1(1-1
38	28	100.0	17	5	AAB47685	Aab47685 SDF-1(1-8
39	28	100.0	17	5	AAB47713	Aab47713 SDF-1(1-8
40	28	100.0	17	5	AAB47681	Aab47681 SDF-1(1-1
41	28	100.0	17	5	AAM48661	Aam48661 CXCR4 pep
42	28	100.0	17	5	AAM48664	Aam48664 CXCR4 pep
43	28	100.0	18	5	AAM48663	Aam48663 CXCR4 pep
44	28	100.0	18	9	AEC75678	Aec75678 Human str
45	28	100.0	19	5	AAB47683	Aab47683 SDF-1(1-9

ALIGNMENTS

RESULT 1

ID	ADU18132	standard; peptide; 6 AA.
XX		
AC	ADU18132;	
XX		
DT	27-JAN-2005	(first entry)
XX		
DE	Immune cell potentiating factor peptide #3.	
XX		
KW	immunostimulant; cytostatic; antimicrobial; antibacterial; virucide;	
KW	antiparasitic; antitubercular; tuberculostatic; immune modulation;	
KW	bacterial infection; viral infection; parasitic infection; cancer;	
KW	neoplasia; bioterrorism; surgery; post-operative infection;	
KW	vaccine adjuvant; immune cell potentiating factor.	
XX		
OS	Capra hircus.	
XX		
PN	WO2004094455-A2.	
XX		
PD	04-NOV-2004.	
XX		
PF	16-APR-2004; 2004WO-US011896.	
XX		
PR	16-APR-2003; 2003US-0463042P.	
XX		
PA	(GENE-) GENEBACT BIOTECHNOLOGIES INC.	
XX		
PI	Thacker JD, Fuhrer PJ, Willeford KO;	
XX		
DR	WPI; 2004-795526/78.	
XX		
PT	New isolated peptides having an amino terminus and a carboxy terminus	
PT	useful for the treatment or prevention of viral and bacterial infections,	
PT	comprise amino acids as given in the specification.	
XX		
PS	Claim 14; SEQ ID NO 3; 55pp; English.	
XX		
CC	The invention relates to an isolated peptide having an amino terminus and	
CC	a carboxy terminus, selected from four amino acid sequences (A1), (A2),	
CC	(A3) and (A4), respectively, (A1; ADU18132), (A2; ADU18131), (A3;	
CC	ADU18134) and H2N-Arg-Ser(-O-R1)-Val-Leu-Ser-Tyr(-H2N-Phe-O-CH2(-	
CC	CH(-CH2-O-R3)-O-R2))-Phe-O-CH2(-CH2-O-R3)-O-R2) (A4; ADU18130),	
CC	respectively where R1-R3 are fatty acid groups (preferably stearic acid,	
CC	arachidic acid or arachidonic acid). The peptides can be used for the	
CC	treatment or prevention of a mammalian disease or disorder such as,	

CC bacterial, viral or parasitic infections and/or cancer or neoplasia, such
 CC as cholera, dysentery, influenza and tuberculosis, as a prophylactic for
 CC short term protection in a bioterrorism area and other contagion envions
 CC and in patients undergoing major surgery to prevent post-operative
 CC infections, as a vaccine adjuvant to provide long-term protection, and
 CC also useful in adjunctive therapy. The peptides act as immune cell
 CC potentiating factors (ICPF) i.e. immune regulators, exhibit a broad
 CC spectrum of therapeutic efficiency and a wide margin of safety to the
 CC host species with respect to toxic and fetal side effects, as associated
 CC with the prior art ICPFs. The peptides are effective in an amount that
 CC produces a serum concentration of greater than 1 microgram/ml, and are
 CC capable of providing an affordable therapy for serious infectious
 CC diseases. This sequence corresponds to a peptide of the invention.

XX Sequence 6 AA;

Query Match 100.0%; Score 28; DB 8; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLSLYR 6
 |||||
 Db 1 VLSLYR 6

RESULT 2

AAV34090
 ID AAV34090 standard; protein; 8 AA.

AC AAV34090;

DT 29-NOV-1999 (first entry)

DE CXCR4 antagonist SDF-1 peptide analogue.

KW CXCR4 chemokine receptor 4; CXCR4; antagonist; medicament; T-cell;
 KW interferon gamma; autoimmune disease; multiple sclerosis; cancer;
 KW angiogenesis; stromal cell derived factor 1; SDF-1.

OS Synthetic.

FX Key Location/Qualifiers

FT Cross-links 8

FT /note= "a lysine residue or a bridge-forming moiety
 FT covalently links this peptide to another peptide of the
 FT same sequence (kgvlslyrc)"

FX WO9947158-A2.

PN 23-SEP-1999.

PD 12-MAR-1999; 99WO-CA000221.

PR 13-MAR-1998; 98CA-02226391.

PR 14-AUG-1998; 98CA-02245224.

PA (UYBR-) UNIV BRITISH COLUMBIA.

XX Clark-Lewis I, Gong J, Duronio V;

XX WPI; 1999-561857/47.

XX Use of CXCR4 chemokine receptor 4 for treating autoimmune disease and
 XX cancer.

PS Disclosure; Fig 14; 71pp; English.

XX The invention relates to the use of a CXCR4 chemokine receptor 4 (CXCR4)
 CC antagonist for the manufacture of a medicament for reducing interferon
 CC gamma production by T-cells in a mammal. The CXCR4 antagonist can be used
 CC to treat or to design a medicament to treat, an autoimmune disease,
 CC multiple sclerosis, cancer, or for inhibiting angiogenesis. The CXCR4
 CC antagonists may be peptide compounds comprising a substantially purified

CC peptide fragment, analogue or a pharmacologically acceptable salt of
 CC stromal cell derived factor 1 (SDF-1). The present sequence represents
 CC the N-terminal fragment of a SDF-1 protein analogue. This fragment can be
 CC used as the CXCR4 antagonist

XX Sequence 8 AA;

Query Match 100.0%; Score 28; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLSLYR 6
 |||||
 Db 3 VLSLYR 8

RESULT 3

AAV67591

ID AAV67591 standard; peptide; 8 AA.

AC AAV67591;

DT 13-JUN-2000 (first entry)

DE SDF-1 N-terminal peptide as CXCR4 antagonist.

KW SDF-1; CXCR4; CXCR4 chemokine receptor 4; gamma-interferon; cancer; gout;
 KW autoimmune disease; multiple sclerosis; rheumatoid arthritis; psoriasis;
 KW type 1 diabetes; ulcerative colitis; lupus; antagonist; antitumour;
 KW stromal cell derived factor one; anti-inflammatory; immunomodulatory.

OS Unidentified.

PN WO200009152-A1.

PD 24-FEB-2000.

PF 16-AUG-1999; 99WO-CA000750.

PR 14-AUG-1998; 98CA-02245224.

XX (UYBR-) UNIV BRITISH COLUMBIA.

XX Clark-Lewis I, Gong J, Duronio V, Salari H;

XX WPI; 2000-224175/19.

XX Therapeutic composition containing CXCR4 antagonist, useful for treating
 XX autoimmune disease, especially multiple sclerosis and cancer.

PS Claim 19; Page 54; 88pp; English.

XX The invention provides a therapeutic composition containing an antagonist
 CC of CXCR4 (CXCR4 chemokine receptor 4) and an excipient. The compositions
 CC are specifically used: to reduce production of gamma-interferon by T
 CC cells, particularly for treating autoimmune disease, especially multiple
 CC sclerosis but also e.g. Guillain-Barre syndrome, amyotrophic lateral
 CC sclerosis, rheumatoid arthritis, psoriasis, type 1 diabetes, ulcerative
 CC colitis, gout, lupus and transplant rejection; to treat cancer by
 CC inhibiting angiogenesis; inhibition of restenosis; and when labeled, to
 CC evaluate in vivo pharmacokinetics, or to determine disease progression
 CC and susceptibility, or as targeting agents for delivery of other
 CC therapeutic agents. The antagonist is selected from SDF-1 (stromal cell
 CC derived factor one) peptide fragments, SDF-1 being the only known natural
 CC ligand for CXCR4. The present sequence represents a SDF-1 peptide that
 CC can be used as a CXCR4 antagonist

XX Sequence 8 AA;

Query Match 100.0%; Score 28; DB 3; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLSYR 6
DB 3 VLSYR 8

RESULT 4
AAB47684
ID AAB47684 standard; peptide; 8 AA.
XX AC AAB47684;
XX DT 30-JAN-2002 (first entry)
XX DE SDF-1(1-8).
XX KW Haematopoietic cell; multiplication; CXC chemokine receptor 4; CXCR4;
KW agonist; stromal cell derived factor one; SDF-1; autoimmune disease;
KW macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer; autologous;
KW allogenic; bone marrow; stem cell; transplantation.
XX OS Synthetic.
XX PN WO200176615-A2.
XX PD 18-OCT-2001.
XX PF 12-APR-2001; 2001WO-CA000540.
XX PR 12-APR-2000; 2000CA-02305036.
XX PR 14-SEP-2000; 2000US-0232425P.
XX PR 23-FEB-2001; 2001CA-02335109.
XX PA (UYBR-) UNIV BRITISH COLUMBIA.
XX PA (CHEN-) CHEMOKINE THERAPEUTICS CORP.
XX PI Salari H, Merzouk A, Arab L, Tudan CR, Saxena G, Eaves CJ;
PI Cashman J, Clark-Lewis I;
XX WPI; 2002-0259882/03.
XX CXC receptor 4 agonists that reduces hematopoietic cell multiplication
PT and susceptibility to cytotoxic agents, are useful for bone marrow or
PT peripheral blood stem cell transplantation.
XX Claim 8; Page 57; 74pp; English.
XX The sequences given in AAB47680-717 represent peptides which may be used
CC in the method of the invention for reducing the rate of hematopoietic
CC cell multiplication. These peptides act as CXC chemokine receptor 4
CC (CXCR4) agonists to the cells. These peptides are based on stromal cell
CC derived factor one (SDF-1) with some also containing sequences derived
CC from macrophage inflammatory protein 1-alpha (MIP-1-alpha). They can be
CC used to reduce susceptibility of hematopoietic cells to a cytotoxic
CC agent, by administering one of the agonist peptides to the cells prior to
CC or during exposure of the cells to the cytotoxic agent. The CXCR4 agonist
CC is used to reduce susceptibility of hematopoietic cells to a cytotoxic
CC agent, particularly in a patient with cancer requiring autologous or
CC allogenic bone marrow or peripheral blood stem cell transplantation, or
CC an autoimmune disease
XX SQ Sequence 8 AA;
Query Match 100.0%; Score 28; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLSYR 6
DB 3 VLSYR 8

RESULT 5
ADA50222

ID ADA50222 standard; peptide; 8 AA.
XX AC ADA50222;
XX DT 20-NOV-2003 (first entry)
XX DE Mouse SDF-1 peptide Seq ID18.
XX KW DNA expression vector; immune response; immunopotentiating chemokine;
KW immunogenic polypeptide; infectious agent; cancerous cell;
KW immunostimulant; immunosuppressant; cytostatic; gene therapy; cancer;
KW tumour; metastatic cancer; infectious disease; autoimmune disease;
KW stimulating T cell activity; suppressing T cell activity;
KW macrophage inflammatory protein; mouse; murine; SDF-1.
XX OS Mus musculus.
XX PN US6562800-B1.
XX PD 13-MAY-2003.
XX PF 29-OCT-1999; 99US-00430470.
XX PR 30-OCT-1998; 98US-0106506P.
XX PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX PI Mcmillan M;
XX WPI; 2003-584408/55.
XX PT New DNA expression vectors comprising a DNA encoding an
PT immunopotentiating chemokine and a DNA encoding a heterologous
PT immunogenic polypeptide, useful for inducing an immune response, and for
PT treating cancers.
XX PS Disclosure; Col 11; 40pp; English.
XX CC This invention relates to a novel DNA expression vector for inducing an
CC immune response. The DNA expression vector of the invention encodes both
CC an immunopotentiating chemokine sequence as well as an immunogenic
CC polypeptide sequence which is derived from an infectious agent or
CC cancerous cell. The chemokines are preferably selected from the animal to
CC be treated. The vaccine of the invention may have immunostimulant,
CC immunosuppressant and cytostatic activities and used for a form of gene
CC therapy. The expression vector and compositions comprising the vector of
CC the invention may therefore be useful for inducing an immune response in
CC a mammal, and for treating cancers (tumours and metastatic form of
CC cancer), infectious diseases, autoimmune diseases and other diseases that
CC can be alleviated by either stimulating or suppressing T cell activity.
CC The present sequence is that of the mouse SDF-1 peptide which was used
CC during the creation of a DNA expression vector of the invention.
XX SQ Sequence 8 AA;
Query Match 100.0%; Score 28; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLSYR 6
DB 3 VLSYR 8

RESULT 6
AAY34089
ID AAY34089 standard; protein; 9 AA.
XX AC AAY34089;
XX DT 29-NOV-1999 (first entry)
XX DE CXCR4 antagonist SDF-1 peptide analogue.

DR WPI; 2000-224175/19.
 XX
 XX Therapeutic composition containing CXCR4 antagonist, useful for treating
 PT autoimmune disease, especially multiple sclerosis and cancer.
 XX
 XX Claim 20; Page 54; 88pp; English.
 XX
 XX The invention provides a therapeutic composition containing an antagonist
 CC of CXCR4 (CXC chemokine receptor 4) and an excipient. The compositions
 CC are specifically used: to reduce production of gamma-interferon by T
 CC cells, particularly for treating autoimmune disease, especially multiple
 CC sclerosis but also e.g. Guillain-Barre syndrome, amyotrophic lateral
 CC sclerosis, rheumatoid arthritis, psoriasis, type 1 diabetes, ulcerative
 CC colitis, gout, lupus and transplant rejection; to treat cancer by
 CC inhibiting angiogenesis; inhibition of restenosis; and when labeled, to
 CC evaluate in vivo pharmacokinetics, or to determine disease progression
 CC and susceptibility, or as targeting agents for delivery of other
 CC therapeutic agents. The antagonist is selected from SDF-1 (stromal cell
 CC derived factor one) peptide fragments, SDF-1 being the only known natural
 CC ligand for CXCR4. The present sequence represents a SDF-1 peptide that
 CC can be used as a CXCR4 antagonist
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 28; DB 3; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VSLSYR 6
 |||||
 Db 3 VSLSYR 8

RESULT 9
 AAB47711
 ID AAB47711 standard; peptide; 9 AA.
 XX
 AC AAB47711;
 XX
 XX 30-JAN-2002 (first entry)

DE SDF-1(1-9)-2-C9/C9 cysteine dimer.
 XX
 XX Haematopoietic cell; multiplication; CXC chemokine receptor 4; CXCR4;
 KW agonist; stromal cell derived factor one; SDF-1; autoimmune disease;
 KW macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer; autologous;
 KW allogenic; bone marrow; stem cell; transplantation.
 XX
 OS Synthetic.

XX
 XX Key Location/Qualifiers
 FH Cross-links 9
 FT /note= "Binds C9 in identical peptide"
 FT
 XX
 XX WO200176615-A2.
 PN
 XX 18-OCT-2001.

XX 12-APR-2001; 2001WO-CA000540.
 XX
 XX 12-APR-2000; 2000CA-02305036.
 PR
 XX 14-SEP-2000; 2000US-0232425P.
 PR
 XX 23-FEB-2001; 2001CA-02335109.

XX (UYBR-) UNIV BRITISH COLUMBIA.
 PA (CHEM-) CHEMOKINE THERAPEUTICS CORP.
 XX
 XX Salari H, Merzouk A, Arab L, Tudan CR, Saxena G, Eaves CJ;
 PI Cashman J, Clark-Lewis I;
 PI
 XX WPI; 2002-025882/03.
 DR
 XX

PT CXC receptor 4 agonists that reduces hematopoietic cell multiplication

PT and susceptibility to cytotoxic agents, are useful for bone marrow or
 PT peripheral blood stem cell transplantation.
 XX
 XX Example 1; Page 47; 74pp; English.

XX The sequences given in AAB47680-717 represent peptides which may be used
 CC in the method of the invention for reducing the rate of hematopoietic
 CC cell multiplication. These peptides act as CXC chemokine receptor 4
 CC (CXCR4) agonists to the cells. These peptides are based on stromal cell
 CC derived factor one (SDF-1) with some also containing sequences derived
 CC from macrophage inflammatory protein 1-alpha (MIP-1-alpha). They can be
 CC used to reduce susceptibility of hematopoietic cells to a cytotoxic
 CC agent, by administering one of the agonist peptides to the cells prior to
 CC or during exposure of the cells to the cytotoxic agent. The CXCR4 agonist
 CC is used to reduce susceptibility of hematopoietic cells to a cytotoxic
 CC agent, particularly in a patient with cancer requiring autologous or
 CC allogenic bone marrow or peripheral blood stem cell transplantation, or
 CC an autoimmune disease
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 28; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VSLSYR 6
 |||||
 Db 3 VSLSYR 8

RESULT 10
 AAB47682
 ID AAB47682 standard; peptide; 9 AA.
 XX
 AC AAB47682;
 XX
 XX 30-JAN-2002 (first entry)

DE SDF-1(1-9).
 XX
 XX Haematopoietic cell; multiplication; CXC chemokine receptor 4; CXCR4;
 KW agonist; stromal cell derived factor one; SDF-1; autoimmune disease;
 KW macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer; autologous;
 KW allogenic; bone marrow; stem cell; transplantation.

XX Synthetic.
 OS
 XX WO200176615-A2.
 PN
 XX 18-OCT-2001.

XX 12-APR-2001; 2001WO-CA000540.
 XX
 XX 12-APR-2000; 2000CA-02305036.
 PR
 XX 14-SEP-2000; 2000US-0232425P.
 PR
 XX 23-FEB-2001; 2001CA-02335109.

XX (UYBR-) UNIV BRITISH COLUMBIA.
 PA (CHEM-) CHEMOKINE THERAPEUTICS CORP.
 XX
 XX Salari H, Merzouk A, Arab L, Tudan CR, Saxena G, Eaves CJ;
 PI Cashman J, Clark-Lewis I;
 PI
 XX WPI; 2002-025882/03.
 DR
 XX

XX CXC receptor 4 agonists that reduces hematopoietic cell multiplication
 PT and susceptibility to cytotoxic agents, are useful for bone marrow or
 PT peripheral blood stem cell transplantation.
 XX
 XX Claim 8; Page 57; 74pp; English.

XX The sequences given in AAB47680-717 represent peptides which may be used
 CC in the method of the invention for reducing the rate of hematopoietic

CC cell multiplication. These peptides act as CXCR4 chemokine receptor 4
 CC (CXCR4) agonists to the cells. These peptides are based on stromal cell
 CC derived factor one (SDF-1) with some also containing sequences derived
 CC from macrophage inflammatory protein 1-alpha (MIP-1-alpha). They can be
 CC used to reduce susceptibility of hematopoietic cells to a cytotoxic
 CC agent, by administering one of the agonist peptides to the cells prior to
 CC or during exposure of the cells to the cytotoxic agent. The CXCR4 agonist
 CC is used to reduce susceptibility of hematopoietic cells to a cytotoxic
 CC agent, particularly in a patient with cancer requiring autologous or
 CC allogeneic bone marrow or peripheral blood stem cell transplantation, or
 CC an autoimmune disease

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 28; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06; Mismatches 0; Indels 0; Gaps 0;
 Matches 6; Conservative 0;

QY 1 VLSYR 6
 |||||
 Db 3 VLSYR 8

RESULT 11

AAM48662
 ID AAM48662 standard; peptide; 9 AA.

XX AC AAM48662;

XX DT 20-MAY-2002 (first entry)

XX DE CXCR4 peptide antagonist SEQ ID NO 14.

XX KW CRX4; haematopoietic cell; chemokine receptor-4; cytostatic;
 KW immunosuppressive; cancer; autoimmune disease; peripheral blood locus;
 KW cell multiplication.

XX OS Synthetic.

XX PN WO200195196-A2.

XX PD 15-NOV-2001.

XX PF 09-MAY-2001; 2001WO-COA00659.

XX PR 09-MAY-2000; 2000CA-02305787.

XX PR 19-MAY-2000; 2000US-0205467P.

XX PA (UYBR-) UNIV BRITISH COLUMBIA.

XX PA (CHEM-) CHEMOKINE THERAPEUTICS CORP.

XX PI Tudan CR, Merzouk A, Arab L, Saxena G, Eaves CJ, Cashman J;

XX PI Clark-Lewis I, Salari H;

XX DR WPI; 2002-106073/14.

PT Promoting the rate of hematopoietic cell multiplication for treating a
 PT cancer involves administering chemokine receptor antagonist to the cells.

XX PS Disclosure; Page 17; 68pp; English.

XX CC The invention relates to a method of promoting the rate of haematopoietic
 CC cell multiplication comprising administering chemokine receptor-4 (CXCR4)
 CC antagonist (AAM48656-AAM48701) to haematopoietic cells. The antagonist
 CC has cytostatic and immunosuppressive activity and is useful for treating
 CC cancer or autoimmune disease in a patient; to promote the rate of
 CC haematopoietic cell multiplication; to formulate a medication for
 CC increasing the circulation of the haematopoietic cells in a patient;
 CC mobilising haematopoietic cells from a marrow locus to a peripheral blood
 CC locus; in the treatment of haematopoietic cells in vitro and in vivo. The
 CC CXCR4 antagonists stimulate haematopoietic cell multiplication, self-
 CC renewal, expansion and proliferation of peripheralisation in vivo

SQ Sequence 9 AA;

Query Match 100.0%; Score 28; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06; Mismatches 0; Indels 0; Gaps 0;
 Matches 6; Conservative 0;

QY 1 VLSYR 6
 |||||
 Db 3 VLSYR 8

RESULT 12

ADU18130

XX ID ADU18130 standard; peptide; 9 AA.

XX AC ADU18130;

XX DT 27-JAN-2005 (first entry)

XX DE Immune cell potentiating factor peptide #1.

XX KW immunostimulant; cytostatic; antimicrobial; antibacterial; virucide;
 KW antiparasitic; antitubercular; tuberculostatic; immune modulation;
 KW bacterial infection; viral infection; parasitic infection; cancer;
 KW neoplasia; bioterrorism; surgery; post-operative infection;
 KW vaccine adjuvant; immune cell potentiating factor.

XX OS Capra hircus.

XX OS Synthetic.

XX FH Key Location/Qualifiers

XX FT Modified-site 2

XX FT Modified-site 9 /note= "conjugated to fatty acid on the side chain"

XX FT Modified-site 9 /note= "conjugated to fatty acid groups on the side chain
 and the C-terminus"

XX PN WO2004094455-A2.

XX PD 04-NOV-2004.

XX PF 16-APR-2004; 2004WO-US011896.

XX PR 16-APR-2003; 2003US-0463042P.

XX PA (GENE-) GENEACT BIOTECHNOLOGIES INC.

XX PI Thacker JD, Fuhrer PJ, Willeford KO;

XX DR WPI; 2004-795526/78.

XX PT New isolated peptides having an amino terminus and a carboxy terminus
 PT useful for the treatment or prevention of viral and bacterial infections,
 PT comprise amino acids as given in the specification.

XX PS Claim 14; SEQ ID NO 1; 55pp; English.

XX CC The invention relates to an isolated peptide having an amino terminus and
 CC a carboxy terminus, selected from four amino acid sequences (A1), (A2),
 CC (A3) and (A4), respectively, (A1; ADU18132), (A2; ADU18131), (A3;
 CC ADU18134) and H2N-Arg-Ser(-O-R1)-Val-Ser-Leu-Ser-Tyr-Arg(-H2N-Phe-O-CH2(-
 CC CH(-CH2-O-R3)-O-R2))-Phe-O-CH2(-CH(-CH2-O-R3)-O-R2) (A4; ADU18130),
 CC respectively where R1-R3 are fatty acid groups (preferably stearic acid,
 CC arachidic acid or arachidonic acid). The peptides can be used for the
 CC treatment or prevention of a mammalian disease or disorder such as,
 CC bacterial, viral or parasitic infections and/or cancer or neoplasia, such
 CC as cholera, dysentery, influenza and tuberculosis, as a prophylactic for
 CC short term protection in a bioterrorism area and other contagion environs
 CC and in patients undergoing major surgery to prevent post-operative
 CC infections, as a vaccine adjuvant to provide long-term protection, and
 CC also useful in adjunctive therapy. The peptides act as immune cell
 CC potentiating factors (ICPP) i.e. immune regulators, exhibit a broad
 CC spectrum of therapeutic efficiency and a wide margin of safety to the

CC host species with respect to toxic and fetal side effects, as associated
CC with the prior art ICPPs. The peptides are effective in an amount that
CC produces a serum concentration of greater than 1 microgram/ml, and are
CC capable of providing an affordable therapy for serious infectious
CC diseases. This sequence corresponds to a peptide of the invention
CC isolated from goat serum.
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 28; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLSYSR 6
|||
Db 3 VLSYSR 8

RESULT 13

ADU18131
ID ADU18131 standard; peptide; 9 AA.

XX
AC ADU18131;

XX
DT 27-JAN-2005 (first entry)

XX
DE Immune cell potentiating factor peptide #2.

XX immunostimulant; cytostatic; antimicrobial; antibacterial; virucide;
KW antiparasitic; antitubercular; tuberculostatic; immune modulation;
KW bacterial infection; viral infection; parasitic infection; cancer;
KW neoplasia; bioterrorism; surgery; post-operative infection;
KW vaccine adjuvant; immune cell potentiating factor.
XX

OS Capra hircus.

XX WO2004094455-A2.

XX
PD 04-NOV-2004.

XX
PF 16-APR-2004; 2004WO-US011896.

XX
PR 16-APR-2003; 2003US-0463042P.

XX (GENE-) GENEBACT BIOTECHNOLOGIES INC.

XX Thacker JD, Fuhrer PJ, Willeford KO;

XX WPI; 2004-795526/78.

XX
PT New isolated peptides having an amino terminus and a carboxy terminus
PT useful for the treatment or prevention of viral and bacterial infections,
PT comprise amino acids as given in the specification.
XX

PS Claim 8; SEQ ID NO 2; 55pp; English.

XX The invention relates to an isolated peptide having an amino terminus and
CC a carboxy terminus, selected from four amino acid sequences (A1), (A2),
CC (A3) and (A4), respectively, (A1; ADU18132), (A2; ADU18131), (A3;
CC ADU18134) and H2N-Arg-Ser(-O-R1)-Val-Ser-Leu-Ser-Tyr-Arg(-H2N-Phe-O-CH2(-
CC CH(-CH2-O-R3)-O-R2))-Phe-O-CH2(-CH(-CH2-O-R3)-O-R2) (A4; ADU18130),
CC respectively where R1-R3 are fatty acid groups (preferably stearic acid,
CC arachidic acid or arachidonic acid). The peptides can be used for the
CC treatment or prevention of a mammalian disease or disorder such as,
CC bacterial, viral or parasitic infections and/or cancer or neoplasia, such
CC as cholera, dysentery, influenza and tuberculosis, as a prophylactic for
CC short term protection in a bioterrorism area and other contagion environs
CC and in patients undergoing major surgery to prevent post-operative
CC infections, as a vaccine adjuvant to provide long-term protection, and
CC also useful in adjunctive therapy. The peptides act as immune cell
CC potentiating factors (ICPF) i.e. immune regulators, exhibit a broad
CC spectrum of therapeutic efficiency and a wide margin of safety to the
CC host species with respect to toxic and fetal side effects, as associated
CC

CC with the prior art ICPPs. The peptides are effective in an amount that
CC produces a serum concentration of greater than 1 microgram/ml, and are
CC capable of providing an affordable therapy for serious infectious
CC diseases. This sequence corresponds to a peptide of the invention.
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 28; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLSYSR 6
|||
Db 3 VLSYSR 8

RESULT 14

ADU18134

ID ADU18134 standard; peptide; 9 AA.

XX
AC ADU18134;

XX
DT 27-JAN-2005 (first entry)

XX
DE Immune cell potentiating factor peptide #5.

XX immunostimulant; cytostatic; antimicrobial; antibacterial; virucide;
KW antiparasitic; antitubercular; tuberculostatic; immune modulation;
KW bacterial infection; viral infection; parasitic infection; cancer;
KW neoplasia; bioterrorism; surgery; post-operative infection;
KW vaccine adjuvant; immune cell potentiating factor.
XX

OS Capra hircus.

XX Synthetic.

XX WO2004094455-A2.

XX
PD 04-NOV-2004.

XX
PF 16-APR-2004; 2004WO-US011896.

XX
PR 16-APR-2003; 2003US-0463042P.

XX (GENE-) GENEBACT BIOTECHNOLOGIES INC.

XX Thacker JD, Fuhrer PJ, Willeford KO;

XX WPI; 2004-795526/78.

XX
PT New isolated peptides having an amino terminus and a carboxy terminus
PT useful for the treatment or prevention of viral and bacterial infections,
PT comprise amino acids as given in the specification.
XX

PS Claim 12; SEQ ID NO 5; 55pp; English.

XX The invention relates to an isolated peptide having an amino terminus and
CC a carboxy terminus, selected from four amino acid sequences (A1), (A2),
CC (A3) and (A4), respectively, (A1; ADU18132), (A2; ADU18131), (A3;
CC ADU18134) and H2N-Arg-Ser(-O-R1)-Val-Ser-Leu-Ser-Tyr-Arg(-H2N-Phe-O-CH2(-
CC CH(-CH2-O-R3)-O-R2))-Phe-O-CH2(-CH(-CH2-O-R3)-O-R2) (A4; ADU18130),
CC respectively where R1-R3 are fatty acid groups (preferably stearic acid,
CC arachidic acid or arachidonic acid). The peptides can be used for the
CC treatment or prevention of a mammalian disease or disorder such as,
CC bacterial, viral or parasitic infections and/or cancer or neoplasia, such
CC as cholera, dysentery, influenza and tuberculosis, as a prophylactic for
CC short term protection in a bioterrorism area and other contagion environs
CC and in patients undergoing major surgery to prevent post-operative
CC infections, as a vaccine adjuvant to provide long-term protection, and
CC also useful in adjunctive therapy. The peptides act as immune cell
CC potentiating factors (ICPF) i.e. immune regulators, exhibit a broad
CC spectrum of therapeutic efficiency and a wide margin of safety to the
CC host species with respect to toxic and fetal side effects, as associated
CC with the prior art ICPPs. The peptides are effective in an amount that
CC

CC produces a serum concentration of greater than 1 microgram/ml, and are
 CC capable of providing an affordable therapy for serious infectious
 CC diseases. This sequence corresponds to a peptide of the invention.

XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 28; DB 8; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLSYR 6
 |||||
 Db 3 VLSYR 8

RESULT 15

AAAY08416
 ID AAY08416 standard; peptide; 11 AA.

XX
 AC AAY08416;

XX 26-JUL-1999 (first entry)

XX CXCR-4 receptor binding peptide 1.

DE CXCR-4 receptor; antagonist; stroma cell-derived factor-1; SDF-1; HIV-1;
 KW infection; lymphotropic strain; treatment; diagnosis.

XX Synthetic.

XX DE19734161-A1.

XX PD 01-APR-1999.

XX PF 07-AUG-1997; 97DE-01034161.

XX PR 07-AUG-1997; 97DE-01034161.

XX PA (JERI-) JERINI BIOTOOLS GMBH.

XX PI Schneider-Mergener J, Germeroth L, Heveker N, Alison M;

XX WPI; 1999-230182/20.

XX Antagonists of stroma cell-derived factor-1, for diagnosis and treatment
 PT of human immune deficiency virus (HIV) infection.

XX PS Disclosure; Page 12; 20pp; German.

XX This invention describes novel antagonists of stroma cell-derived factor-
 CC 1 (SDF-1) which bind to the CXCR-4 receptor, to which SDF-1 normally
 CC binds, so prevents binding of this receptor to HIV-1, an essential step
 CC in infection by lymphotropic strains of the virus. The peptides of the
 CC invention (AAAY08416-Y08438) are used to treat or diagnose human immune
 CC deficiency virus-1 (HIV-1) infection and provide, for the first time, a
 CC method for antagonizing the interaction between HIV-1 and the CXCR-4
 CC receptor

XX SQ Sequence 11 AA;

Query Match 100.0%; Score 28; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLSYR 6
 |||||
 Db 1 VLSYR 6

Search completed: August 10, 2006, 23:00:40
 Job time : 81.1818 secs